SEQUENCE LISTING

<110> MILLENNIUM PHARMACEUTICALS, INC.
      Cook, William
      Kapeller-Libermann, Rosana

<120> 14790, NOVEL PROTEIN KINASE MOLECULE AND
      USES TREREFOR

<130> 38155-20002.00

<140> US 09/515,806
<141> 2000-02-29

<160> 33

<170> FastSEQ for Windows Version 4.0

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   1   5   10   15

ccg gag agc tac ccg caa cga cag gac cac gag cta cag gcc ctg gag   155
Pro Glu Ser Tyr Pro Gln Arg Gln Asp His Glu Leu Gln Ala Leu Glu
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gcc atc tac ggc gcg gac ttc caa gac ctg cgg ccg gac gct tgc gga   203
Ala Ile Tyr Gly Ala Asp Phe Gln Asp Leu Arg Pro Asp Ala Cys Gly
                35   40   45

ccg gtc aaa gag ccc cct gaa atc aat tta gtt ttg tac cct caa ggc   251
Pro Val Lys Glu Pro Pro Glu Ile Asn Leu Val Leu Tyr Pro Gln Gly
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cta act ggt gaa gaa gta tat gta aaa gtg gat ttg agg gtt aaa tgc   299
Leu Thr Gly Glu Glu Val Tyr Val Lys Val Asp Leu Arg Val Lys Cys
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cca cct acc tat cca gat gta gtt cct gaa ata gag tta aaa aat gcc   347
Pro Pro Thr Tyr Pro Asp Val Val Pro Glu Ile Glu Leu Lys Asn Ala
80   85   90   95

aaa ggt cta tca aat gaa agt gtc aat ttg tta aaa tct cgc cta gaa   395
Lys Gly Leu Ser Asn Glu Ser Val Asn Leu Leu Lys Ser Arg Leu Glu
                100   105   110

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gaa ctg gcc aag aaa cac tgt ggg gag gtg atg atc ttt gaa ctg gct      443
Glu Leu Ala Lys Lys His Cys Gly Glu Val Met Ile Phe Glu Leu Ala
            115             120             125

tac cac gtg cag tca ttt ctc agc gag cat aac aag ccc cct ccc aag      491
Tyr His Val Gln Ser Phe Leu Ser Glu His Asn Lys Pro Pro Pro Lys
            130             135             140

tct ttt cat gaa gaa atg ctg gaa agg cgg gct cag gag gag cag cag      539
Ser Phe His Glu Glu Met Leu Glu Arg Arg Ala Gln Glu Glu Gln Gln
            145             150             155

agg ctg ttg gag gcc aag cgg aaa gaa gag cag gag caa cgt gaa atc      587
Arg Leu Leu Glu Ala Lys Arg Lys Glu Glu Gln Glu Gln Arg Glu Ile
160             165             170             175

ctg cat gag att cag aga agg aaa gaa gag ata aaa gaa gag aaa aaa      635
Leu His Glu Ile Gln Arg Arg Lys Glu Glu Ile Lys Glu Glu Lys Lys
                180             185             190

agg aaa gaa atg gct aag cag gaa cgt ttg gaa att gct agt ttg tca      683
Arg Lys Glu Met Ala Lys Gln Glu Arg Leu Glu Ile Ala Ser Leu Ser
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aac caa gat cat acc tct aag aag gac cca gga gga cac aga acg gct      731
Asn Gln Asp His Thr Ser Lys Lys Asp Pro Gly Gly His Arg Thr Ala
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gcc att cta cat gga ggc tct cct gac ttt gta gga aat ggt aaa cat      779
Ala Ile Leu His Gly Gly Ser Pro Asp Phe Val Gly Asn Gly Lys His
            225             230             235

cgg gca aac tcc tca gga agg tct agg cga gaa cgt cag tat tct gta      827
Arg Ala Asn Ser Ser Gly Arg Ser Arg Arg Glu Arg Gln Tyr Ser Val
240             245             250             255

tgt aat agt gaa gat tct cct ggc tct tgt gaa att ctg tat ttc aat      875
Cys Asn Ser Glu Asp Ser Pro Gly Ser Cys Glu Ile Leu Tyr Phe Asn
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atg ggg agt cct gat cag ctc atg gtg cac aaa ggg aaa tgt att ggc      923
Met Gly Ser Pro Asp Gln Leu Met Val His Lys Gly Lys Cys Ile Gly
                275             280             285

agt gat gaa caa ctt gga aaa tta gtc tac aat gct ttg gaa aca gcc      971
Ser Asp Glu Gln Leu Gly Lys Leu Val Tyr Asn Ala Leu Glu Thr Ala
                290             295             300

act ggt ggc ttt gtc ttg ttg tat gag tgg gtc ctt cag tgg cag aaa     1019
Thr Gly Gly Phe Val Leu Leu Tyr Glu Trp Val Leu Gln Trp Gln Lys
            305             310             315

aaa atg ggt cca ttc ctt acc agt caa gaa aaa gag aag att gat aag     1067
Lys Met Gly Pro Phe Leu Thr Ser Gln Glu Lys Glu Lys Ile Asp Lys
320             325             330             335

tgc aaa aag cag att caa gga aca gaa aca gaa ttc aac tca ctg gta     1115
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2

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Lys Leu Ser His Pro Asn Val Val Arg Tyr Leu Ala Met Asn Leu Lys
                355             360             365

gag caa gac gac tcc atc gtg gtg gac att tta gtg gag cac att agt          1211
Glu Gln Asp Asp Ser Ile Val Val Asp Ile Leu Val Glu His Ile Ser
                370             375             380

ggg gtc tct ctt gct gca cac ctg agc cac tca ggc ccc atc cct gtg          1259
Gly Val Ser Leu Ala Ala His Leu Ser His Ser Gly Pro Ile Pro Val
            385             390             395

cat cag ctt cgc agg tac aca gct cag ctc ctg tca ggc ctt gat tat          1307
His Gln Leu Arg Arg Tyr Thr Ala Gln Leu Leu Ser Gly Leu Asp Tyr
400             405             410             415

ctg cac agc aat tct gtg gtg cat aag gtc ctg agt gca tct aat gtc          1355
Leu His Ser Asn Ser Val Val His Lys Val Leu Ser Ala Ser Asn Val
                420             425             430

ttg gtg gat gca gaa ggc acc gtc aag att acg gac tat agc att tct          1403
Leu Val Asp Ala Glu Gly Thr Val Lys Ile Thr Asp Tyr Ser Ile Ser
            435             440             445

aag cgc ctc gca gac att tgc aag gag gat gtg ttt gag caa acc cga          1451
Lys Arg Leu Ala Asp Ile Cys Lys Glu Asp Val Phe Glu Gln Thr Arg
                450             455             460

gtt cgt ttt agt gac aat gct ctg cct tat aaa acg ggg aag aaa gga          1499
Val Arg Phe Ser Asp Asn Ala Leu Pro Tyr Lys Thr Gly Lys Lys Gly
            465             470             475

gat gtt tgg cgt ctt ggc ctt ctg ctg ctg tcc ctc agc caa gga cag          1547
Asp Val Trp Arg Leu Gly Leu Leu Leu Leu Ser Leu Ser Gln Gly Gln
480             485             490             495

gaa tgt gga gag tac cct gtg acc atc cct agt gac tta cca gct gac          1595
Glu Cys Gly Glu Tyr Pro Val Thr Ile Pro Ser Asp Leu Pro Ala Asp
                500             505             510

ttt caa gat ttt cta aag aaa tgt gtg tgc ttg gat gac aag gaa aga          1643
Phe Gln Asp Phe Leu Lys Lys Cys Val Cys Leu Asp Asp Lys Glu Arg
                515             520             525

tgg agt ccc cag cag ttg ttg aaa cac agc ttt ata aat ccc cag cca          1691
Trp Ser Pro Gln Gln Leu Leu Lys His Ser Phe Ile Asn Pro Gln Pro
                530             535             540

aaa atg cct cta gtg gaa caa agt cct gaa gat tct gga gga caa gat          1739
Lys Met Pro Leu Val Glu Gln Ser Pro Glu Asp Ser Gly Gly Gln Asp
                545             550             555

tat gtt gag act gtt att cct agc aac cgg cta ccc agt gct gcc ttc          1787
Tyr Val Glu Thr Val Ile Pro Ser Asn Arg Leu Pro Ser Ala Ala Phe
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3

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        560                    565                     570                     575

ttt agt gag aca cag aga cag ttt tcc cga tac ttc att gag ttt gaa        1835
Phe Ser Glu Thr Gln Arg Gln Phe Ser Arg Tyr Phe Ile Glu Phe Glu
                580                     585                     590

gaa tta caa ctt ctt ggt aaa gga gct ttt gga gct gtc atc aag gtg        1883
Glu Leu Gln Leu Leu Gly Lys Gly Ala Phe Gly Ala Val Ile Lys Val
                595                     600                     605

cag aac aag ttg gac ggc tgc tgc tac gca gtg aag cgc atc ccc atc        1931
Gln Asn Lys Leu Asp Gly Cys Cys Tyr Ala Val Lys Arg Ile Pro Ile
                610                     615                     620

aac ccg gcc agc cgg cag ttc cgc agg atc aag ggc gaa gtg aca ctg        1979
Asn Pro Ala Ser Arg Gln Phe Arg Arg Ile Lys Gly Glu Val Thr Leu
                625                     630                     635

ctg tca cgg ctg cac cat gag aac att gtg cgc tac tac aac gcc tgg        2027
Leu Ser Arg Leu His His Glu Asn Ile Val Arg Tyr Tyr Asn Ala Trp
640                     645                     650                     655

atc gag cgg cac gag cgg ccg gcg gga ccg ggg acg ccg ccc ccg gac        2075
Ile Glu Arg His Glu Arg Pro Ala Gly Pro Gly Thr Pro Pro Pro Asp
                660                     665                     670

tcc ggg ccc ctg gcc aag gat gac cga gct gca cgc ggg cag ccg gcg        2123
Ser Gly Pro Leu Ala Lys Asp Asp Arg Ala Ala Arg Gly Gln Pro Ala
                675                     680                     685

agc gac aca gac ggc ctg gac agc gta gag gcc gcc gcg ccg cca ccc        2171
Ser Asp Thr Asp Gly Leu Asp Ser Val Glu Ala Ala Ala Pro Pro Pro
                690                     695                     700

atc ctc agc agc tcg gtg gag tgg agc act tcg ggc gag cgc tcg gcc        2219
Ile Leu Ser Ser Ser Val Glu Trp Ser Thr Ser Gly Glu Arg Ser Ala
                705                     710                     715

agt gcc cgt ttc ccc gcc acc ggc ccg ggc tcc agc gat gac gag gac        2267
Ser Ala Arg Phe Pro Ala Thr Gly Pro Gly Ser Ser Asp Asp Glu Asp
720                     725                     730                     735

gac gac gag gac gag cac ggt ggc gtc ttc tcc cag tcc ttc ctg cct        2315
Asp Asp Glu Asp Glu His Gly Gly Val Phe Ser Gln Ser Phe Leu Pro
                740                     745                     750

gct tca gat tct gaa agt gat att atc ttt gac aat gaa gat gag aac        2363
Ala Ser Asp Ser Glu Ser Asp Ile Ile Phe Asp Asn Glu Asp Glu Asn
                755                     760                     765

agt aaa agt cag aat cag gat gaa gat tgc aat gaa aag aat ggc tgc        2411
Ser Lys Ser Gln Asn Gln Asp Glu Asp Cys Asn Glu Lys Asn Gly Cys
                770                     775                     780

cat gaa agt gag cca tca gtg acg act gag gct gtg cac tac cta tac        2459
His Glu Ser Glu Pro Ser Val Thr Thr Glu Ala Val His Tyr Leu Tyr
                785                     790                     795
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4

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atc cag atg gag tac tgt gag aag agc act tta cga gac acc att gac      2507
Ile Gln Met Glu Tyr Cys Glu Lys Ser Thr Leu Arg Asp Thr Ile Asp
800                 805                 810                 815

cag gga ctg tat cga gac acc gtc aga ctc tgg agg ctt ttt cga gag      2555
Gln Gly Leu Tyr Arg Asp Thr Val Arg Leu Trp Arg Leu Phe Arg Glu
                820                 825                 830

att ctg gat gga tta gct tat atc cat gag aaa gga atg att cac cgg      2603
Ile Leu Asp Gly Leu Ala Tyr Ile His Glu Lys Gly Met Ile His Arg
                835                 840                 845

gat ttg aag cct gtc aac att ttt ttg gat tct gat gac cat gtg aaa      2651
Asp Leu Lys Pro Val Asn Ile Phe Leu Asp Ser Asp Asp His Val Lys
                850                 855                 860

ata ggt gat ttt ggt ttg gcg aca gac cat cta gcc ttt tct gct gac      2699
Ile Gly Asp Phe Gly Leu Ala Thr Asp His Leu Ala Phe Ser Ala Asp
        865                 870                 875

agc aaa caa gac gat cag aca gga gac ttg att aag tca gac cct tca      2747
Ser Lys Gln Asp Asp Gln Thr Gly Asp Leu Ile Lys Ser Asp Pro Ser
880                 885                 890                 895

ggt cac tta act ggg atg gtt ggc act gct ctc tat gta agc cca gag      2795
Gly His Leu Thr Gly Met Val Gly Thr Ala Leu Tyr Val Ser Pro Glu
                900                 905                 910

gtc caa gga agc acc aaa tct gca tac aac cag aaa gtg gat ctc ttc      2843
Val Gln Gly Ser Thr Lys Ser Ala Tyr Asn Gln Lys Val Asp Leu Phe
                915                 920                 925

agc ctg gga att atc ttc ttt gag atg tcc tat cac ccc atg gtc acg      2891
Ser Leu Gly Ile Ile Phe Phe Glu Met Ser Tyr His Pro Met Val Thr
                930                 935                 940

gct tca gaa agg atc ttt gtt ctc aac caa ctc aga gat ccc act tcg      2939
Ala Ser Glu Arg Ile Phe Val Leu Asn Gln Leu Arg Asp Pro Thr Ser
        945                 950                 955

cct aag ttt cca gaa gac ttt gac gat gga gag cat gca aag cag aaa      2987
Pro Lys Phe Pro Glu Asp Phe Asp Asp Gly Glu His Ala Lys Gln Lys
960                 965                 970                 975

tca gtc atc tcc tgg ctg ttg aac cac gat cca gca aaa cgg ccc aca      3035
Ser Val Ile Ser Trp Leu Leu Asn His Asp Pro Ala Lys Arg Pro Thr
                980                 985                 990

gcc aca gaa ctg ctc aag agt gag ctg ctg ccc cca ccc cag atg gag      3083
Ala Thr Glu Leu Leu Lys Ser Glu Leu Leu Pro Pro Pro Gln Met Glu
                995                 1000                1005

gag tca gag ctg cat gaa gtg ctg cac cac acg ctg acc aac gtg gat      3131
Glu Ser Glu Leu His Glu Val Leu His His Thr Leu Thr Asn Val Asp
                1010                1015                1020
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ggg aag gcc tac cgc acc atg atg gcc cag atc ttc tcg cag cgc atc        3179
Gly Lys Ala Tyr Arg Thr Met Met Ala Gln Ile Phe Ser Gln Arg Ile
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tcc cct gcc atc gat tac acc tat gac agc gac ata ctg aag ggc aac        3227
Ser Pro Ala Ile Asp Tyr Thr Tyr Asp Ser Asp Ile Leu Lys Gly Asn
1040                1045                1050                1055

ttc tca atc cgt aca gcc aag atg cag cag cat gtg tgt gaa acc atc        3275
Phe Ser Ile Arg Thr Ala Lys Met Gln Gln His Val Cys Glu Thr Ile
            1060                1065                1070

atc cgc atc ttt aaa aga cat gga gct gtt cag ttg tgt act cca cta        3323
Ile Arg Ile Phe Lys Arg His Gly Ala Val Gln Leu Cys Thr Pro Leu
            1075                1080                1085

ctg ctt ccc cga aac aga caa ata tat gag cac aac gaa gct gcc cta        3371
Leu Leu Pro Arg Asn Arg Gln Ile Tyr Glu His Asn Glu Ala Ala Leu
            1090                1095                1100

ttc atg gac cac agc ggg atg ctg gtg atg ctt cct ttt gac ctg cgg        3419
Phe Met Asp His Ser Gly Met Leu Val Met Leu Pro Phe Asp Leu Arg
            1105                1110                1115

atc cct ttt gca aga tat gtg gca aga aat aat ata ttg aat tta aaa        3467
Ile Pro Phe Ala Arg Tyr Val Ala Arg Asn Asn Ile Leu Asn Leu Lys
1120                1125                1130                1135

cga tac tgc ata gaa cgt gtg ttc agg ccg cgc aag tta gat cga ttt        3515
Arg Tyr Cys Ile Glu Arg Val Phe Arg Pro Arg Lys Leu Asp Arg Phe
            1140                1145                1150

cat ccc aaa gaa ctt ctg gag tgt gca ttt gat att gtc act tct acc        3563
His Pro Lys Glu Leu Leu Glu Cys Ala Phe Asp Ile Val Thr Ser Thr
            1155                1160                1165

acc aac agc ttt ctg ccc act gct gaa att atc tac act atc tat gaa        3611
Thr Asn Ser Phe Leu Pro Thr Ala Glu Ile Ile Tyr Thr Ile Tyr Glu
            1170                1175                1180

atc atc caa gag ttt cca gca ctt cag gaa aga aat tac agt att tat        3659
Ile Ile Gln Glu Phe Pro Ala Leu Gln Glu Arg Asn Tyr Ser Ile Tyr
    1185                1190                1195

ttg aac cat acc atg tta ttg aaa gca ata ctc tta cac tgt ggg atc        3707
Leu Asn His Thr Met Leu Leu Lys Ala Ile Leu Leu His Cys Gly Ile
1200                1205                1210                1215

cca gaa gat aaa ctc agt caa gtc tac att att ctg tat gat gct gtg        3755
Pro Glu Asp Lys Leu Ser Gln Val Tyr Ile Ile Leu Tyr Asp Ala Val
                1220                1225                1230

aca gag aag ctg acg agg aga gaa gtg gaa gct aaa ttt tgt aat ctg        3803
Thr Glu Lys Leu Thr Arg Arg Glu Val Glu Ala Lys Phe Cys Asn Leu
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tct ttg tct tct aat agt ctg tgt cga ctc tac aag ttt att gaa cag        3851
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6

Ser Leu Ser Ser Asn Ser Leu Cys Arg Leu Tyr Lys Phe Ile Glu Gln
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aag gga gat ttg caa gat ctt atg cca aca ata aat tca tta ata aaa   3899
Lys Gly Asp Leu Gln Asp Leu Met Pro Thr Ile Asn Ser Leu Ile Lys
    1265   1270   1275

cag aaa aca ggt att gca cag ttg gtg aag tat ggc tta aaa gac cta   3947
Gln Lys Thr Gly Ile Ala Gln Leu Val Lys Tyr Gly Leu Lys Asp Leu
1280   1285   1290   1295

gag gag gtt gtt gga ctg ttg aag aaa ctc ggc atc aag tta cag gtc   3995
Glu Glu Val Val Gly Leu Leu Lys Lys Leu Gly Ile Lys Leu Gln Val
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ttg atc aat ttg ggc ttg gtt tac aag gtg cag cag cac aat gga atc   4043
Leu Ile Asn Leu Gly Leu Val Tyr Lys Val Gln Gln His Asn Gly Ile
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atc ttc cag ttt gtg gct ttc atc aaa cga agg caa agg gct gta cct   4091
Ile Phe Gln Phe Val Ala Phe Ile Lys Arg Arg Gln Arg Ala Val Pro
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gaa atc ctc gca gct gga ggc aga tat gac ctg ctg att ccc cag ttt   4139
Glu Ile Leu Ala Ala Gly Gly Arg Tyr Asp Leu Leu Ile Pro Gln Phe
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aga ggg cca caa gct ctg ggg cca gtt ccc act gcc att ggg gtc agc   4187
Arg Gly Pro Gln Ala Leu Gly Pro Val Pro Thr Ala Ile Gly Val Ser
1360   1365   1370   1375

ata gct ata gac aag ata tct gct gct gtc ctc aac atg gag gaa tct   4235
Ile Ala Ile Asp Lys Ile Ser Ala Ala Val Leu Asn Met Glu Glu Ser
                  1380   1385   1390

gtt aca ata agc tct tgt gac ctc ctg gtt gta agt gtt ggt cag atg   4283
Val Thr Ile Ser Ser Cys Asp Leu Leu Val Val Ser Val Gly Gln Met
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tct atg tcc agg gcc atc aac cta acc cag aaa ctc tgg aca gca ggc   4331
Ser Met Ser Arg Ala Ile Asn Leu Thr Gln Lys Leu Trp Thr Ala Gly
                  1410   1415   1420

atc aca gca gaa atc atg tac gac tgg tca cag tcc caa gag gaa tta   4379
Ile Thr Ala Glu Ile Met Tyr Asp Trp Ser Gln Ser Gln Glu Glu Leu
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caa gag tac tgc aga cat cat gaa atc acc tat gtg gcc ctt gtc tcg   4427
Gln Glu Tyr Cys Arg His His Glu Ile Thr Tyr Val Ala Leu Val Ser
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gat aaa gaa gga agc cat gtc aag gtt aag tct ttc gag aag gaa agg   4475
Asp Lys Glu Gly Ser His Val Lys Val Lys Ser Phe Glu Lys Glu Arg
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cag aca gag aag cgt gtg ctg gag act gaa ctt gtg gac cat gta ctg   4523
Gln Thr Glu Lys Arg Val Leu Glu Thr Glu Leu Val Asp His Val Leu

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cag aaa ctg agg act aaa gtc act gat gaa agg aat ggc aga gaa gct     4571
Gln Lys Leu Arg Thr Lys Val Thr Asp Glu Arg Asn Gly Arg Glu Ala
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tcc gat aat ctt gca gtg caa aat ctg aag ggg tca ttt tct aat gct     4619
Ser Asp Asn Leu Ala Val Gln Asn Leu Lys Gly Ser Phe Ser Asn Ala
        1505            1510            1515

tca ggt ttg ttt gaa atc cat gga gca aca gtg gtt ccc att gtg agt     4667
Ser Gly Leu Phe Glu Ile His Gly Ala Thr Val Val Pro Ile Val Ser
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gtg cta gcc ccg gag aag ctg tca gcc agc act agg agg cgc tat gaa     4715
Val Leu Ala Pro Glu Lys Leu Ser Ala Ser Thr Arg Arg Arg Tyr Glu
                1540            1545            1550

act cag gta caa act cga ctt cag acc tcc ctt gcc aac tta cat cag     4763
Thr Gln Val Gln Thr Arg Leu Gln Thr Ser Leu Ala Asn Leu His Gln
            1555            1560            1565

aaa agc agt gaa att gaa att ctg gct gtg gat cta ccc aaa gaa aca     4811
Lys Ser Ser Glu Ile Glu Ile Leu Ala Val Asp Leu Pro Lys Glu Thr
        1570            1575            1580

ata tta cag ttt tta tca tta gag tgg gat gct gat gaa cag gca ttt     4859
Ile Leu Gln Phe Leu Ser Leu Glu Trp Asp Ala Asp Glu Gln Ala Phe
        1585            1590            1595

aac aca act gtg aag cag ctg ctg tca cgc ctg cca aag caa aga tac     4907
Asn Thr Thr Val Lys Gln Leu Leu Ser Arg Leu Pro Lys Gln Arg Tyr
1600            1605            1610            1615

ctc aaa tta gtc tgt gat gaa att tat aac atc aaa gta gaa aaa aag     4955
Leu Lys Leu Val Cys Asp Glu Ile Tyr Asn Ile Lys Val Glu Lys Lys
                1620            1625            1630

gtg tct gtg cta ttt ctg tac agc tat aga gat gac tac tac aga atc     5003
Val Ser Val Leu Phe Leu Tyr Ser Tyr Arg Asp Asp Tyr Tyr Arg Ile
        1635            1640            1645

tta ttt taa ccctaaagaa ctgtcgttaa cctcattcaa acagacagag           5052
Leu Phe  *
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<212> PRT
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            20              25              30
Ile Tyr Gly Ala Asp Phe Gln Asp Leu Arg Pro Asp Ala Cys Gly Pro
        35              40              45
Val Lys Glu Pro Pro Glu Ile Asn Leu Val Leu Tyr Pro Gln Gly Leu
    50              55              60
Thr Gly Glu Glu Val Tyr Val Lys Val Asp Leu Arg Val Lys Cys Pro
65              70              75              80
Pro Thr Tyr Pro Asp Val Val Pro Glu Ile Glu Leu Lys Asn Ala Lys
            85              90              95
Gly Leu Ser Asn Glu Ser Val Asn Leu Leu Lys Ser Arg Leu Glu Glu
            100             105             110
Leu Ala Lys Lys His Cys Gly Glu Val Met Ile Phe Glu Leu Ala Tyr
        115             120             125
His Val Gln Ser Phe Leu Ser Glu His Asn Lys Pro Pro Pro Lys Ser
    130             135             140
Phe His Glu Glu Met Leu Glu Arg Arg Ala Gln Glu Glu Gln Gln Arg
145             150             155             160
Leu Leu Glu Ala Lys Arg Lys Glu Glu Gln Glu Gln Arg Glu Ile Leu
            165             170             175
His Glu Ile Gln Arg Arg Lys Glu Glu Ile Lys Glu Glu Lys Lys Arg
            180             185             190
Lys Glu Met Ala Lys Gln Glu Arg Leu Glu Ile Ala Ser Leu Ser Asn
        195             200             205
Gln Asp His Thr Ser Lys Lys Asp Pro Gly Gly His Arg Thr Ala Ala
    210             215             220
Ile Leu His Gly Gly Ser Pro Asp Phe Val Gly Asn Gly Lys His Arg
225             230             235             240
Ala Asn Ser Ser Gly Arg Ser Arg Arg Glu Arg Gln Tyr Ser Val Cys
            245             250             255
Asn Ser Glu Asp Ser Pro Gly Ser Cys Glu Ile Leu Tyr Phe Asn Met
            260             265             270
Gly Ser Pro Asp Gln Leu Met Val His Lys Gly Lys Cys Ile Gly Ser
        275             280             285
Asp Glu Gln Leu Gly Lys Leu Val Tyr Asn Ala Leu Glu Thr Ala Thr
    290             295             300
Gly Gly Phe Val Leu Leu Tyr Glu Trp Val Leu Gln Trp Gln Lys Lys
305             310             315             320
Met Gly Pro Phe Leu Thr Ser Gln Glu Lys Glu Lys Ile Asp Lys Cys
            325             330             335
Lys Lys Gln Ile Gln Gly Thr Glu Thr Glu Phe Asn Ser Leu Val Lys
            340             345             350
Leu Ser His Pro Asn Val Val Arg Tyr Leu Ala Met Asn Leu Lys Glu
        355             360             365
Gln Asp Asp Ser Ile Val Val Asp Ile Leu Val Glu His Ile Ser Gly
    370             375             380
Val Ser Leu Ala Ala His Leu Ser His Ser Gly Pro Ile Pro Val His
385             390             395             400
Gln Leu Arg Arg Tyr Thr Ala Gln Leu Leu Ser Gly Leu Asp Tyr Leu
            405             410             415
His Ser Asn Ser Val Val His Lys Val Leu Ser Ala Ser Asn Val Leu
```

9

```
                420                      425                      430
Val Asp Ala Glu Gly Thr Val Lys Ile Thr Asp Tyr Ser Ile Ser Lys
            435                      440                      445
Arg Leu Ala Asp Ile Cys Lys Glu Asp Val Phe Glu Gln Thr Arg Val
        450                      455                      460
Arg Phe Ser Asp Asn Ala Leu Pro Tyr Lys Thr Gly Lys Lys Gly Asp
465                      470                      475                      480
Val Trp Arg Leu Gly Leu Leu Leu Leu Ser Leu Ser Gln Gly Gln Glu
                    485                      490                      495
Cys Gly Glu Tyr Pro Val Thr Ile Pro Ser Asp Leu Pro Ala Asp Phe
            500                      505                      510
Gln Asp Phe Leu Lys Lys Cys Val Cys Leu Asp Asp Lys Glu Arg Trp
        515                      520                      525
Ser Pro Gln Gln Leu Leu Lys His Ser Phe Ile Asn Pro Gln Pro Lys
    530                      535                      540
Met Pro Leu Val Glu Gln Ser Pro Glu Asp Ser Gly Gly Gln Asp Tyr
545                      550                      555                      560
Val Glu Thr Val Ile Pro Ser Asn Arg Leu Pro Ser Ala Ala Phe Phe
                    565                      570                      575
Ser Glu Thr Gln Arg Gln Phe Ser Arg Tyr Phe Ile Glu Phe Glu Glu
            580                      585                      590
Leu Gln Leu Leu Gly Lys Gly Ala Phe Gly Ala Val Ile Lys Val Gln
        595                      600                      605
Asn Lys Leu Asp Gly Cys Cys Tyr Ala Val Lys Arg Ile Pro Ile Asn
    610                      615                      620
Pro Ala Ser Arg Gln Phe Arg Arg Ile Lys Gly Glu Val Thr Leu Leu
625                      630                      635                      640
Ser Arg Leu His His Glu Asn Ile Val Arg Tyr Tyr Asn Ala Trp Ile
                    645                      650                      655
Glu Arg His Glu Arg Pro Ala Gly Pro Gly Thr Pro Pro Pro Asp Ser
            660                      665                      670
Gly Pro Leu Ala Lys Asp Asp Arg Ala Ala Arg Gly Gln Pro Ala Ser
        675                      680                      685
Asp Thr Asp Gly Leu Asp Ser Val Glu Ala Ala Ala Pro Pro Pro Ile
    690                      695                      700
Leu Ser Ser Ser Val Glu Trp Ser Thr Ser Gly Glu Arg Ser Ala Ser
705                      710                      715                      720
Ala Arg Phe Pro Ala Thr Gly Pro Gly Ser Ser Asp Asp Glu Asp Asp
                    725                      730                      735
Asp Glu Asp Glu His Gly Gly Val Phe Ser Gln Ser Phe Leu Pro Ala
            740                      745                      750
Ser Asp Ser Glu Ser Asp Ile Ile Phe Asp Asn Glu Asp Glu Asn Ser
        755                      760                      765
Lys Ser Gln Asn Gln Asp Glu Asp Cys Asn Glu Lys Asn Gly Cys His
    770                      775                      780
Glu Ser Glu Pro Ser Val Thr Thr Glu Ala Val His Tyr Leu Tyr Ile
785                      790                      795                      800
Gln Met Glu Tyr Cys Glu Lys Ser Thr Leu Arg Asp Thr Ile Asp Gln
                    805                      810                      815
Gly Leu Tyr Arg Asp Thr Val Arg Leu Trp Arg Leu Phe Arg Glu Ile
            820                      825                      830
Leu Asp Gly Leu Ala Tyr Ile His Glu Lys Gly Met Ile His Arg Asp
        835                      840                      845
Leu Lys Pro Val Asn Ile Phe Leu Asp Ser Asp Asp His Val Lys Ile
    850                      855                      860
Gly Asp Phe Gly Leu Ala Thr Asp His Leu Ala Phe Ser Ala Asp Ser
865                      870                      875                      880
```

10

```
Lys Gln Asp Asp Gln Thr Gly Asp Leu Ile Lys Ser Asp Pro Ser Gly
            885                     890                     895
His Leu Thr Gly Met Val Gly Thr Ala Leu Tyr Val Ser Pro Glu Val
            900                     905                     910
Gln Gly Ser Thr Lys Ser Ala Tyr Asn Gln Lys Val Asp Leu Phe Ser
            915                     920                     925
Leu Gly Ile Ile Phe Phe Glu Met Ser Tyr His Pro Met Val Thr Ala
            930                     935                     940
Ser Glu Arg Ile Phe Val Leu Asn Gln Leu Arg Asp Pro Thr Ser Pro
945                     950                     955                     960
Lys Phe Pro Glu Asp Phe Asp Asp Gly Glu His Ala Lys Gln Lys Ser
                        965                     970                     975
Val Ile Ser Trp Leu Leu Asn His Asp Pro Ala Lys Arg Pro Thr Ala
            980                     985                     990
Thr Glu Leu Leu Lys Ser Glu Leu Leu Pro Pro Pro Gln Met Glu Glu
            995                     1000                    1005
Ser Glu Leu His Glu Val Leu His His Thr Leu Thr Asn Val Asp Gly
            1010                    1015                    1020
Lys Ala Tyr Arg Thr Met Met Ala Gln Ile Phe Ser Gln Arg Ile Ser
1025                    1030                    1035                    1040
Pro Ala Ile Asp Tyr Thr Tyr Asp Ser Asp Ile Leu Lys Gly Asn Phe
                        1045                    1050                    1055
Ser Ile Arg Thr Ala Lys Met Gln Gln His Val Cys Glu Thr Ile Ile
                        1060                    1065                    1070
Arg Ile Phe Lys Arg His Gly Ala Val Gln Leu Cys Thr Pro Leu Leu
                        1075                    1080                    1085
Leu Pro Arg Asn Arg Gln Ile Tyr Glu His Asn Glu Ala Ala Leu Phe
            1090                    1095                    1100
Met Asp His Ser Gly Met Leu Val Met Leu Pro Phe Asp Leu Arg Ile
1105                    1110                    1115                    1120
Pro Phe Ala Arg Tyr Val Ala Arg Asn Asn Ile Leu Asn Leu Lys Arg
                        1125                    1130                    1135
Tyr Cys Ile Glu Arg Val Phe Arg Pro Arg Lys Leu Asp Arg Phe His
                        1140                    1145                    1150
Pro Lys Glu Leu Leu Glu Cys Ala Phe Asp Ile Val Thr Ser Thr Thr
                        1155                    1160                    1165
Asn Ser Phe Leu Pro Thr Ala Glu Ile Ile Tyr Thr Ile Tyr Glu Ile
            1170                    1175                    1180
Ile Gln Glu Phe Pro Ala Leu Gln Glu Arg Asn Tyr Ser Ile Tyr Leu
1185                    1190                    1195                    1200
Asn His Thr Met Leu Leu Lys Ala Ile Leu Leu His Cys Gly Ile Pro
                        1205                    1210                    1215
Glu Asp Lys Leu Ser Gln Val Tyr Ile Ile Leu Tyr Asp Ala Val Thr
                        1220                    1225                    1230
Glu Lys Leu Thr Arg Arg Glu Val Glu Ala Lys Phe Cys Asn Leu Ser
                        1235                    1240                    1245
Leu Ser Ser Asn Ser Leu Cys Arg Leu Tyr Lys Phe Ile Glu Gln Lys
            1250                    1255                    1260
Gly Asp Leu Gln Asp Leu Met Pro Thr Ile Asn Ser Leu Ile Lys Gln
1265                    1270                    1275                    1280
Lys Thr Gly Ile Ala Gln Leu Val Lys Tyr Gly Leu Lys Asp Leu Glu
                        1285                    1290                    1295
Glu Val Val Gly Leu Leu Lys Lys Leu Gly Ile Lys Leu Gln Val Leu
            1300                    1305                    1310
Ile Asn Leu Gly Leu Val Tyr Lys Val Gln Gln His Asn Gly Ile Ile
            1315                    1320                    1325
Phe Gln Phe Val Ala Phe Ile Lys Arg Arg Gln Arg Ala Val Pro Glu
```

11

```
        1330                    1335                    1340
Ile Leu Ala Ala Gly Gly Arg Tyr Asp Leu Leu Ile Pro Gln Phe Arg
1345                    1350                    1355                    1360
Gly Pro Gln Ala Leu Gly Pro Val Pro Thr Ala Ile Gly Val Ser Ile
            1365                    1370                    1375
Ala Ile Asp Lys Ile Ser Ala Ala Val Leu Asn Met Glu Glu Ser Val
                1380                    1385                    1390
Thr Ile Ser Ser Cys Asp Leu Leu Val Val Ser Val Gly Gln Met Ser
            1395                    1400                    1405
Met Ser Arg Ala Ile Asn Leu Thr Gln Lys Leu Trp Thr Ala Gly Ile
        1410                    1415                    1420
Thr Ala Glu Ile Met Tyr Asp Trp Ser Gln Ser Gln Glu Glu Leu Gln
1425                    1430                    1435                    1440
Glu Tyr Cys Arg His His Glu Ile Thr Tyr Val Ala Leu Val Ser Asp
                1445                    1450                    1455
Lys Glu Gly Ser His Val Lys Val Lys Ser Phe Glu Lys Glu Arg Gln
                1460                    1465                    1470
Thr Glu Lys Arg Val Leu Glu Thr Glu Leu Val Asp His Val Leu Gln
                1475                    1480                    1485
Lys Leu Arg Thr Lys Val Thr Asp Glu Arg Asn Gly Arg Glu Ala Ser
            1490                    1495                    1500
Asp Asn Leu Ala Val Gln Asn Leu Lys Gly Ser Phe Ser Asn Ala Ser
1505                    1510                    1515                    1520
Gly Leu Phe Glu Ile His Gly Ala Thr Val Val Pro Ile Val Ser Val
                1525                    1530                    1535
Leu Ala Pro Glu Lys Leu Ser Ala Ser Thr Arg Arg Arg Tyr Glu Thr
            1540                    1545                    1550
Gln Val Gln Thr Arg Leu Gln Thr Ser Leu Ala Asn Leu His Gln Lys
            1555                    1560                    1565
Ser Ser Glu Ile Glu Ile Leu Ala Val Asp Leu Pro Lys Glu Thr Ile
        1570                    1575                    1580
Leu Gln Phe Leu Ser Leu Glu Trp Asp Ala Asp Glu Gln Ala Phe Asn
1585                    1590                    1595                    1600
Thr Thr Val Lys Gln Leu Leu Ser Arg Leu Pro Lys Gln Arg Tyr Leu
            1605                    1610                    1615
Lys Leu Val Cys Asp Glu Ile Tyr Asn Ile Lys Val Glu Lys Lys Val
            1620                    1625                    1630
Ser Val Leu Phe Leu Tyr Ser Tyr Arg Asp Asp Tyr Tyr Arg Ile Leu
            1635                    1640                    1645
Phe
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<210> 3
<211> 4950
<212> DNA
<213> Homo sapiens

<400> 3
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caacgacagg accacgagct acaggccctg gaggccatct acggcgcgga cttccaagac     120
ctgcggccgg acgcttgcgg accggtcaaa gagcccctg aaatcaattt agttttgtac      180
cctcaaggcc taactggtga agaagtatat gtaaaagtgg atttgagggt taaatgccca     240
cctacctatc cagatgtagt tcctgaaata gagttaaaaa atgccaaagg tctatcaaat     300
gaaagtgtca atttgttaaa atctcgccta gaagaactgg ccaagaaaca ctgtggggag     360
gtgatgatct ttgaactggc ttaccacgtg cagtcatttc tcagcgagca taacaagccc     420
cctcccaagt cttttcatga agaaatgctg gaaaggcggg ctcaggagga gcagcagagg     480
ctgttggagg ccaagcggaa agaagagcag gagcaacgtg aaatcctgca tgagattcag     540
```

```
agaaggaaag aagagataaa agaagagaaa aaaaggaaag aaatggctaa gcaggaacgt    600
ttggaaattg ctagtttgtc aaaccaagat catacctcta agaaggaccc aggaggacac    660
agaacggctg ccattctaca tggaggctct cctgactttg taggaaatgg taaacatcgg    720
gcaaactcct caggaaggtc taggcgagaa cgtcagtatt ctgtatgtaa tagtgaagat    780
tctcctggct cttgtgaaat tctgtatttc aatatgggga gtcctgatca gctcatggtg    840
cacaaaggga aatgtattgg cagtgatgaa caacttggaa aattagtcta caatgctttg    900
gaaacagcca ctggtggctt tgtcttgttg tatgagtggg tccttcagtg gcagaaaaaa    960
atgggtccat tccttaccag tcaagaaaaa gagaagattg ataagtgcaa aaagcagatt   1020
caaggaacag aaacagaatt caactcactg gtaaaattga gccatccaaa tgtagtacgc   1080
taccttgcaa tgaatctcaa agagcaagac gactccatcg tggtggacat tttagtggag   1140
cacattagtg gggtctctct tgctgcacac ctgagccact caggccccat ccctgtgcat   1200
cagcttcgca ggtacacagc tcagctcctg tcaggccttg attatctgca cagcaattct   1260
gtggtgcata aggtcctgag tgcatctaat gtcttggtgg atgcagaagg caccgtcaag   1320
attacggact atagcatttc taagcgcctc gcagacattt gcaaggagga tgtgtttgag   1380
caaacccgag ttcgttttag tgacaatgct ctgccttata aaacggggaa gaaaggagat   1440
gtttggcgtc ttggccttct gctgctgtcc ctcagccaag gacaggaatg tggagagtac   1500
cctgtgacca tccctagtga cttaccagct gactttcaag attttctaaa gaaatgtgtg   1560
tgcttggatg acaaggaaag atggagtccc cagcagttgt tgaaacacag ctttataaat   1620
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atccccatca acccggccag ccggcagttc cgcaggatca agggcgaagt gacactgctg   1920
tcacggctgc accatgagaa cattgtgcgc tactacaacg cctggatcga gcggcacgag   1980
cggccggcgg gaccggggac gccgcccccg gactccgggc ccctggccaa ggatgaccga   2040
gctgcacgcg ggcagccggc gagcgacaca gacggcctgg acagcgtaga ggccgccgcg   2100
ccgccaccca tcctcagcag ctcggtggag tggagcactt cgggcgagcg ctcggccagt   2160
gcccgtttcc ccgccaccgg cccgggctcc agcgatgacg aggacgacga cgaggacgag   2220
cacggtggcg tcttctccca gtccttcctg cctgcttcag attctgaaag tgatattatc   2280
tttgacaatg aagatgagaa cagtaaaagt cagaatcagg atgaagattg caatgaaaag   2340
aatggctgcc atgaaagtga gccatcagtg acgactgagg ctgtgcacta cctatacatc   2400
cagatggagt actgtgagaa gagcactta cgagacacca ttgaccaggg actgtatcga   2460
gacaccgtca gactctggag gcttttttcga gagattctgg atggattagc ttatatccat   2520
gagaaaggaa tgattcaccg ggatttgaag cctgtcaaca tttttttgga ttctgatgac   2580
catgtgaaaa taggtgattt tggtttggcg acagaccatc tagcctttc tgctgacagc   2640
aaacaagacg atcagacagg agacttgatt aagtcagacc cttcaggtca cttaactggg   2700
atggttggca ctgctctcta tgtaagccca gaggtccaag gaagcaccaa atctgcatac   2760
aaccagaaag tggatctctt cagcctggga attatcttct ttgagatgtc ctatcacccc   2820
atggtcacgg cttcagaaag gatctttgtt ctcaaccaac tcagagatcc cacttcgcct   2880
aagtttccag aagactttga cgatggagag catgcaaagc agaaatcagt catctcctgg   2940
ctgttgaacc acgatccagc aaaaacggcc cacagccacag aactgctcaa gagtgagctg   3000
ctgcccccac cccagatgga ggagtcagag ctgcatgaag tgctgcacca cacgctgacc   3060
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gccaagatgc agcagcatgt gtgtgaaacc atcatccgca tctttaaaag acatggagct   3240
gttcagttgt gtactccact actgcttccc cgaaacagac aaatatatga gcacaacgaa   3300
gctgccctat tcatggacca cagcgggatg ctggtgatgc ttccttttga cctgcggatc   3360
ccttttgcaa gatatgtggc aagaaataat atattgaatt taaaacgata ctgcatagaa   3420
cgtgtgttca ggccgcgcaa gttagatcga tttcatccca aagaacttct ggagtgtgca   3480
tttgatattg tcacttctac caccaacagc tttctgccca ctgctgaaat tatctacact   3540
atctatgaaa tcatccaaga gtttccagca cttcaggaaa gaaattacag tatttatttg   3600
aaccatacca tgttattgaa agcaatactc ttacactgtg ggatcccaga agataaactc   3660
agtcaagtct acattattct gtatgatgct gtgacagaga agctgacgag gagagaagtg   3720
gaagctaaat tttgtaatct gtctttgtct tctaatagtc tgtgtcgact ctacaagttt   3780
attgaacaga agggagattt gcaagatctt atgccaacaa taaattcatt aataaaacag   3840
aaaacaggta ttgcacagtt ggtgaagtat ggcttaaaag acctagagga ggttgttgga   3900
ctgttgaaga aactcggcat caagttacag gtcttgatca atttgggctt ggtttacaag   3960
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13

```
gtgcagcagc acaatggaat catcttccag tttgtggctt tcatcaaacg aaggcaaagg   4020
gctgtacctg aaatcctcgc agctggaggc agatatgacc tgctgattcc ccagtttaga   4080
gggccacaag ctctggggcc agttcccact gccattgggg tcagcatagc tatagacaag   4140
atatctgctg ctgtcctcaa catggaggaa tctgttacaa taagctcttg tgacctcctg   4200
gttgtaagtg ttggtcagat gtctatgtcc agggccatca acctaaccca gaaactctgg   4260
acagcaggca tcacagcaga aatcatgtac gactggtcac agtcccaaga ggaattacaa   4320
gagtactgca gacatcatga aatcacctat gtggcccttg tctcggataa agaaggaagc   4380
catgtcaagg ttaagtcttt cgagaaggaa aggcagacag agaagcgtgt gctggagact   4440
gaacttgtgg accatgtact gcagaaactg aggactaaag tcactgatga aaggaatggc   4500
agagaagctt ccgataatct tgcagtgcaa aatctgaagg ggtcattttc taatgcttca   4560
ggtttgtttg aaatccatgg agcaacagtg gttcccattg tgagtgtgct agccccggag   4620
aagctgtcag ccagcactag gaggcgctat gaaactcagg tacaaactcg acttcagacc   4680
tcccttgcca acttacatca gaaaagcagt gaaattgaaa ttctggctgt ggatctaccc   4740
aaagaaacaa tattacagtt tttatcatta gagtgggatg ctgatgaaca ggcatttaac   4800
acaactgtga agcagctgct gtcacgcctg ccaaagcaaa gatacctcaa attagtctgt   4860
gatgaaattt ataacatcaa agtagaaaaa aaggtgtctg tgctatttct gtacagctat   4920
agagatgact actacagaat cttatttttaa                                   4950
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<210> 4
<211> 1648
<212> PRT
<213> Homo sapiens

<400> 4

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Met Ala Gly Gly Arg Gly Ala Pro Gly Arg Gly Arg Asp Glu Pro Pro
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Glu Ser Tyr Pro Gln Arg Gln Asp His Glu Leu Gln Ala Leu Glu Ala
                20                  25                  30
Ile Tyr Gly Ala Asp Phe Gln Asp Leu Arg Pro Asp Ala Cys Gly Pro
            35                  40                  45
Val Lys Glu Pro Pro Glu Ile Asn Leu Val Leu Tyr Pro Gln Gly Leu
        50                  55                  60
Thr Gly Glu Glu Val Tyr Val Lys Val Asp Leu Arg Val Lys Cys Pro
65                  70                  75                  80
Pro Thr Tyr Pro Asp Val Val Pro Glu Ile Glu Leu Lys Asn Ala Lys
                85                  90                  95
Gly Leu Ser Asn Glu Ser Val Asn Leu Leu Lys Ser Arg Leu Glu Glu
            100                 105                 110
Leu Ala Lys Lys His Cys Gly Glu Val Met Ile Phe Glu Leu Ala Tyr
            115                 120                 125
His Val Gln Ser Phe Leu Ser Glu His Asn Lys Pro Pro Pro Lys Ser
        130                 135                 140
Phe His Glu Glu Met Leu Glu Arg Arg Ala Gln Glu Glu Gln Gln Arg
145                 150                 155                 160
Leu Leu Glu Ala Arg Arg Lys Glu Glu Gln Glu Gln Arg Glu Ile Leu
                165                 170                 175
His Glu Ile Gln Arg Arg Lys Glu Glu Ile Lys Glu Glu Lys Lys Arg
            180                 185                 190
Lys Glu Met Ala Lys Gln Glu Arg Leu Glu Ile Thr Ser Leu Ser Asn
        195                 200                 205
Gln Asp His Thr Ser Lys Lys Asp Pro Gly Gly His Arg Thr Ala Ala
        210                 215                 220
Ile Leu His Gly Gly Ser Pro Asp Phe Val Gly Asn Gly Lys His Arg
225                 230                 235                 240
Ala Asn Ser Ser Gly Arg Ser Arg Arg Glu Arg Gln Tyr Ser Val Cys
                245                 250                 255
```

14

```
Asn Ser Glu Asp Ser Pro Gly Ser Cys Glu Ile Leu Tyr Phe Asn Met
            260                 265                 270
Gly Ser Pro Asp Gln Leu Met Val His Lys Gly Arg Cys Ile Gly Ser
        275                 280                 285
Asp Glu Gln Leu Gly Lys Leu Val Tyr Asn Ala Leu Glu Thr Ala Thr
    290                 295                 300
Gly Gly Phe Val Leu Leu Tyr Glu Trp Val Leu Gln Trp Gln Lys Met
305                 310                 315                 320
Gly Pro Phe Leu Thr Ser Gln Glu Lys Glu Lys Ile Asp Lys Cys Lys
                325                 330                 335
Lys Gln Ile Gln Gly Tyr Glu Thr Glu Phe Asn Ser Leu Val Lys Leu
            340                 345                 350
Ser His Pro Asn Val Val Arg Tyr Leu Ala Met Asn Leu Lys Glu Gln
        355                 360                 365
Asp Asp Ser Ile Val Val Asp Ile Leu Val Glu His Ile Ser Gly Val
    370                 375                 380
Ser Leu Ala Ala His Leu Ser His Ser Gly Pro Ile Pro Val His Gln
385                 390                 395                 400
Leu Arg Arg Tyr Thr Ala Gln Leu Leu Ser Gly Leu Asp Tyr Leu His
                405                 410                 415
Ser Asn Ser Val Val His Lys Val Leu Ser Ala Ser Asn Val Leu Val
            420                 425                 430
Asp Ala Glu Gly Thr Val Lys Ile Thr Asp Tyr Ser Ile Ser Lys Arg
        435                 440                 445
Leu Ala Asp Ile Cys Lys Glu Asp Val Phe Glu Gln Thr Arg Val Arg
    450                 455                 460
Phe Ser Asp Asn Ala Leu Pro Tyr Lys Thr Gly Lys Lys Gly Asp Val
465                 470                 475                 480
Trp Arg Leu Gly Leu Leu Leu Leu Ser Leu Ser Gln Gly Gln Glu Cys
                485                 490                 495
Gly Glu Tyr Pro Val Thr Ile Pro Ser Asp Leu Pro Ala Asp Phe Gln
            500                 505                 510
Asp Phe Leu Lys Lys Cys Val Cys Leu Asp Asp Lys Glu Arg Trp Ser
        515                 520                 525
Pro Gln Gln Leu Leu Lys His Ser Phe Ile Asn Pro Gln Pro Lys Met
    530                 535                 540
Pro Leu Val Glu Gln Ser Pro Glu Asp Ser Gly Gly Gln Asp Tyr Val
545                 550                 555                 560
Glu Thr Val Ile Pro Ser Asn Arg Leu Pro Ser Ala Ala Phe Phe Ser
                565                 570                 575
Glu Thr Gln Arg Gln Phe Ser Arg Tyr Phe Ile Glu Phe Glu Glu Leu
            580                 585                 590
Gln Leu Leu Gly Lys Gly Ala Phe Gly Ala Val Ile Lys Val Gln Asn
            595                 600                 605
Lys Leu Asp Gly Cys Cys Tyr Ala Val Lys Arg Ile Pro Ile Asn Pro
    610                 615                 620
Ala Ser Arg Gln Phe Arg Arg Ile Lys Gly Glu Val Thr Leu Leu Ser
625                 630                 635                 640
Arg Leu His His Glu Asn Ile Val Arg Tyr Tyr Asn Ala Trp Ile Glu
                645                 650                 655
Arg His Glu Arg Pro Ala Gly Pro Gly Thr Pro Pro Pro Asp Ser Gly
            660                 665                 670
Pro Leu Ala Lys Asp Asp Arg Ala Ala Arg Gly Gln Pro Ala Ser Asp
            675                 680                 685
Thr Asp Gly Leu Asp Ser Val Glu Ala Ala Ala Pro Pro Pro Ile Leu
    690                 695                 700
Ser Ser Ser Val Glu Trp Ser Thr Ser Gly Glu Arg Ser Ala Ser Ala
```

15

```
705                    710                    715                    720
Arg Phe Pro Ala Thr Gly Pro Gly Ser Ser Asp Asp Glu Asp Asp Glu
                    725                    730                    735
Asp Glu His Gly Gly Val Phe Ser Gln Ser Phe Leu Pro Ala Ser Asp
                    740                    745                    750
Ser Glu Ser Asp Ile Ile Phe Asp Asn Glu Asp Glu Asn Ser Lys Ser
                    755                    760                    765
Gln Asn Gln Asp Glu Asp Cys Asn Glu Lys Asn Gly Cys His Glu Ser
                    770                    775                    780
Glu Pro Ser Val Thr Thr Glu Ala Val His Tyr Leu Tyr Ile Gln Met
785                    790                    795                    800
Glu Tyr Cys Glu Lys Ser Thr Leu Arg Asp Thr Ile Asp Gln Gly Leu
                    805                    810                    815
Tyr Arg Asp Thr Val Arg Leu Trp Arg Leu Phe Arg Glu Ile Leu Asp
                    820                    825                    830
Gly Leu Ala Tyr Ile His Glu Lys Gly Met Ile His Arg Asp Leu Lys
                    835                    840                    845
Pro Val Asn Ile Phe Leu Asp Ser Asp Asp His Val Lys Ile Gly Asp
                    850                    855                    860
Phe Gly Leu Ala Thr Asp His Leu Ala Phe Ser Ala Asp Ser Lys Gln
865                    870                    875                    880
Asp Asp Gln Thr Gly Asp Gly Leu Ile Lys Ser Asp Pro Ser Gly His
                    885                    890                    895
Leu Thr Gly Met Val Gly Thr Ala Leu Tyr Val Ser Pro Glu Val Gln
                    900                    905                    910
Gly Ser Thr Lys Ser Ala Tyr Asn Gln Lys Val Asp Leu Phe Ser Leu
                    915                    920                    925
Gly Ile Ile Phe Phe Glu Met Ser Tyr His Pro Met Val Thr Ala Ser
                    930                    935                    940
Glu Arg Ile Phe Val Leu Asn Gln Leu Arg Asp Pro Thr Ser Pro Lys
945                    950                    955                    960
Phe Pro Glu Asp Phe Asp Asp Gly Glu His Ala Lys Gln Lys Ser Val
                    965                    970                    975
Ile Ser Trp Leu Leu Asn His Asp Pro Ala Lys Arg Pro Thr Ala Thr
                    980                    985                    990
Glu Leu Leu Lys Ser Glu Leu Leu Pro Pro Pro Gln Met Glu Glu Ser
                    995                    1000                   1005
Glu Leu His Glu Val Leu His His Thr Leu Thr Asn Val Asp Gly Lys
                    1010                   1015                   1020
Ala Tyr Arg Thr Met Met Ala Gln Ile Phe Ser Gln Arg Ile Ser Pro
1025                   1030                   1035                   1040
Ala Ile Asp Tyr Thr Tyr Asp Ser Asp Ile Leu Lys Gly Asn Phe Ser
                    1045                   1050                   1055
Ile Arg Thr Ala Lys Met Gln Gln His Val Cys Glu Thr Ile Ile Arg
                    1060                   1065                   1070
Ile Phe Lys Arg His Gly Ala Val Gln Leu Cys Thr Pro Leu Leu Leu
                    1075                   1080                   1085
Pro Arg Asn Arg Gln Ile Tyr Glu His Asn Glu Ala Ala Leu Phe Met
                    1090                   1095                   1100
Asp His Ser Gly Met Leu Val Met Leu Pro Phe Asp Leu Arg Ile Pro
1105                   1110                   1115                   1120
Phe Ala Arg Tyr Val Ala Arg Asn Asn Ile Leu Asn Leu Lys Arg Tyr
                    1125                   1130                   1135
Cys Ile Glu Arg Val Phe Arg Pro Arg Lys Leu Asp Arg Phe His Pro
                    1140                   1145                   1150
Lys Glu Leu Leu Glu Cys Ala Phe Asp Ile Val Thr Ser Thr Thr Asn
                    1155                   1160                   1165
```

16

Ser Phe Leu Pro Thr Ala Glu Ile Ile Tyr Thr Ile Tyr Glu Ile Ile
    1170   1175   1180
Gln Glu Phe Pro Ala Leu Gln Glu Arg Asn Tyr Ser Ile Tyr Leu Asn
1185   1190   1195   1200
His Thr Met Leu Leu Lys Ala Ile Leu Leu His Cys Gly Ile Pro Glu
            1205   1210   1215
Asp Lys Leu Ser Gln Val Tyr Ile Ile Leu Tyr Asp Ala Val Thr Glu
            1220   1225   1230
Lys Leu Thr Arg Arg Glu Val Glu Ala Lys Phe Cys Asn Leu Ser Leu
            1235   1240   1245
Ser Ser Asn Ser Leu Cys Arg Leu Tyr Lys Phe Ile Glu Gln Lys Gly
            1250   1255   1260
Asp Leu Gln Asp Leu Met Pro Thr Ile Asn Ser Leu Ile Lys Gln Lys
1265   1270   1275   1280
Thr Gly Ile Ala Gln Leu Val Lys Tyr Ser Leu Lys Asp Leu Glu Asp
            1285   1290   1295
Val Val Gly Leu Leu Lys Lys Leu Gly Ile Lys Leu Gln Val Leu Ile
            1300   1305   1310
Asn Leu Gly Leu Val Tyr Lys Val Gln Gln His Asn Gly Ile Ile Phe
            1315   1320   1325
Gln Phe Val Ala Phe Ile Lys Arg Arg Gln Arg Ala Val Pro Glu Ile
            1330   1335   1340
Leu Ala Ala Gly Gly Arg Tyr Asp Leu Leu Ile Pro Gln Phe Arg Gly
1345   1350   1355   1360
Pro Gln Ala Leu Gly Pro Val Pro Thr Ala Ile Gly Val Ser Ile Ala
            1365   1370   1375
Ile Asp Lys Ile Ser Ala Ala Val Leu Asn Met Glu Glu Ser Val Thr
            1380   1385   1390
Ile Ser Ser Cys Asp Leu Leu Val Val Ser Val Gly Gln Met Ser Met
            1395   1400   1405
Ser Arg Ala Ile Asn Leu Thr Gln Lys Leu Trp Thr Ala Gly Ile Thr
1410   1415   1420
Ala Glu Ile Met Tyr Asp Trp Ser Gln Ser Gln Glu Glu Leu Gln Glu
1425   1430   1435   1440
Tyr Cys Arg His His Glu Ile Thr Tyr Val Ala Leu Val Ser Asp Lys
            1445   1450   1455
Glu Gly Ser His Val Lys Val Lys Ser Phe Glu Lys Glu Arg Gln Thr
            1460   1465   1470
Glu Lys Arg Val Leu Glu Thr Glu Leu Val Asp His Val Leu Gln Lys
            1475   1480   1485
Leu Arg Thr Lys Val Thr Asp Glu Arg Asn Gly Arg Glu Ala Ser Asp
            1490   1495   1500
Asn Leu Ala Val Gln Asn Leu Lys Gly Ser Phe Ser Asn Ala Ser Gly
1505   1510   1515   1520
Leu Phe Glu Ile His Gly Ala Thr Val Val Pro Ile Val Ser Val Leu
            1525   1530   1535
Ala Pro Glu Lys Leu Ser Ala Ser Thr Arg Arg Arg Tyr Glu Ile Gln
            1540   1545   1550
Val Gln Thr Arg Leu Gln Thr Ser Leu Ala Asn Leu His Gln Lys Ser
            1555   1560   1565
Ser Glu Ile Glu Ile Leu Ala Val Asp Leu Pro Lys Glu Thr Ile Leu
            1570   1575   1580
Gln Phe Leu Ser Leu Glu Trp Asp Ala Asp Glu Gln Ala Phe Asn Thr
1585   1590   1595   1600
Thr Val Lys Gln Leu Leu Ser Arg Leu Pro Lys Gln Arg Tyr Leu Lys
            1605   1610   1615
Leu Val Cys Asp Glu Ile Tyr Asn Ile Lys Val Glu Lys Lys Val Ser

17

```
                1620                    1625                    1630
      Val Leu Phe Leu Tyr Ser Tyr Arg Asp Asp Tyr Tyr Arg Ile Leu Phe
                1635                    1640                    1645


<210> 5
<211> 1648
<212> PRT
<213> Mouse


<400> 5
Met Ala Gly Gly Arg Gly Ala Ser Gly Arg Gly Arg Ala Glu Pro Gln
1                 5                  10                  15
Glu Ser Tyr Ser Gln Arg Gln Asp His Glu Leu Gln Ala Leu Glu Ala
            20                  25                  30
Ile Tyr Gly Ser Asp Phe Gln Asp Leu Arg Pro Asp Ala Arg Gly Arg
            35                  40                  45
Val Arg Glu Pro Pro Glu Ile Asn Leu Val Leu Tyr Pro Gln Gly Leu
       50                  55                  60
Ala Gly Glu Glu Val Tyr Val Gln Val Glu Leu Gln Val Lys Cys Pro
65                  70                  75                  80
Pro Thr Tyr Pro Asp Val Val Pro Glu Ile Glu Leu Lys Asn Ala Lys
                85                  90                  95
Gly Leu Ser Asn Glu Ser Val Asn Leu Leu Lys Ser His Leu Glu Glu
            100                 105                 110
Leu Ala Lys Lys Gln Cys Gly Glu Val Met Ile Phe Glu Leu Ala His
            115                 120                 125
His Val Gln Ser Phe Leu Ser Glu His Asn Lys Pro Pro Pro Lys Ser
    130                 135                 140
Phe His Glu Glu Met Leu Glu Arg Gln Ala Gln Glu Lys Gln Gln Arg
145                 150                 155                 160
Leu Leu Glu Ala Arg Arg Lys Glu Glu Gln Glu Gln Arg Glu Ile Leu
                165                 170                 175
His Glu Ile Gln Arg Arg Lys Glu Glu Ile Lys Glu Glu Lys Lys Arg
            180                 185                 190
Lys Glu Met Ala Lys Gln Glu Arg Leu Glu Ile Thr Ser Leu Thr Asn
            195                 200                 205
Gln Asp Tyr Ala Ser Lys Arg Asp Pro Ala Gly His Arg Ala Ala Ala
    210                 215                 220
Ile Leu His Gly Gly Ser Pro Asp Phe Val Gly Asn Gly Lys Ala Arg
225                 230                 235                 240
Thr Tyr Ser Ser Gly Arg Ser Arg Arg Glu Arg Gln Tyr Ser Val Cys
                245                 250                 255
Ser Gly Glu Pro Ser Pro Gly Ser Cys Asp Ile Leu His Phe Ser Val
            260                 265                 270
Gly Ser Pro Asp Gln Leu Met Val His Lys Gly Arg Cys Val Gly Ser
            275                 280                 285
Asp Glu Gln Leu Gly Lys Val Val Tyr Asn Ala Leu Glu Thr Ala Thr
    290                 295                 300
Gly Ser Phe Val Leu Leu His Glu Trp Val Leu Gln Trp Gln Lys Met
305                 310                 315                 320
Gly Pro Cys Leu Thr Ser Gln Glu Lys Glu Lys Ile Asp Lys Cys Lys
                325                 330                 335
Arg Gln Ile Gln Gly Ala Glu Thr Glu Phe Ser Ser Leu Val Lys Leu
            340                 345                 350
Ser His Pro Asn Ile Val Arg Tyr Phe Ala Met Asn Ser Arg Glu Glu
    355                 360                 365
Glu Asp Ser Ile Val Ile Asp Ile Leu Ala Glu His Val Ser Gly Ile
```

18

```
              370                    375                    380
Ser Leu Ala Thr His Leu Ser His Ser Gly Pro Val Pro Ala His Gln
385                    390                    395                    400
Leu Arg Lys Tyr Thr Ala Gln Leu Leu Ala Gly Leu Asp Tyr Leu His
                   405                    410                    415
Ser Asn Ser Val Val His Lys Val Leu Ser Ala Ser Ser Val Leu Val
                   420                    425                    430
Asp Ala Glu Gly Thr Val Lys Ile Thr Asp Tyr Ser Ile Ser Lys Arg
                   435                    440                    445
Leu Ala Asp Ile Cys Lys Glu Asp Val Phe Glu Gln Ala Arg Val Arg
                   450                    455                    460
Phe Ser Asp Ser Ala Leu Pro Tyr Lys Thr Gly Lys Lys Gly Asp Val
465                    470                    475                    480
Trp Arg Leu Gly Leu Leu Leu Leu Ser Leu Ser Gln Gly Gln Glu Cys
                   485                    490                    495
Gly Glu Tyr Pro Val Thr Ile Pro Ser Asp Leu Pro Ala Asp Phe Gln
                   500                    505                    510
Asp Phe Leu Lys Lys Cys Val Cys Leu Asp Asp Lys Glu Arg Trp Ser
                   515                    520                    525
Pro Gln Gln Leu Leu Lys His Ser Phe Ile Asn Pro Gln Pro Lys Leu
                   530                    535                    540
Pro Leu Val Glu Gln Ser Pro Glu Asp Ser Gly Gly Gln Asp Tyr Ile
545                    550                    555                    560
Glu Thr Val Ile Pro Ser Asn Gln Leu Pro Ser Ala Ala Phe Phe Ser
                   565                    570                    575
Glu Thr Gln Lys Gln Phe Ser Arg Tyr Phe Ile Glu Phe Glu Glu Leu
                   580                    585                    590
Gln Leu Leu Gly Lys Gly Ala Phe Gly Ala Val Ile Lys Val Gln Asn
                   595                    600                    605
Lys Leu Asp Gly Cys Cys Tyr Ala Val Lys Arg Ile Pro Ile Asn Pro
                   610                    615                    620
Ala Ser Arg His Phe Arg Arg Ile Lys Gly Glu Val Thr Leu Leu Ser
625                    630                    635                    640
Arg Leu His His Glu Asn Ile Val Arg Tyr Tyr Asn Ala Trp Ile Glu
                   645                    650                    655
Arg His Glu Arg Pro Ala Val Pro Gly Thr Pro Pro Asp Cys Thr
                   660                    665                    670
Pro Gln Ala Gln Asp Ser Pro Ala Thr Cys Gly Lys Thr Ser Gly Asp
                   675                    680                    685
Thr Glu Glu Leu Gly Ser Val Glu Ala Ala Ala Pro Pro Pro Ile Leu
                   690                    695                    700
Ser Ser Ser Val Glu Trp Ser Thr Ser Ala Glu Arg Ser Thr Ser Thr
705                    710                    715                    720
Arg Phe Pro Val Thr Gly Gln Asp Ser Ser Ser Asp Glu Glu Asp Glu
                   725                    730                    735
Asp Glu Arg Asp Gly Val Phe Ser Gln Ser Phe Leu Pro Ala Ser Asp
                   740                    745                    750
Ser Asp Ser Asp Ile Ile Phe Asp Asn Glu Asp Glu Asn Ser Lys Ser
                   755                    760                    765
Gln Asn Gln Asp Glu Asp Cys Asn Gln Lys Asp Gly Ser His Glu Ile
                   770                    775                    780
Glu Pro Ser Val Thr Ala Glu Ala Val His Tyr Leu Tyr Ile Gln Met
785                    790                    795                    800
Glu Tyr Cys Glu Lys Ser Thr Leu Arg Asp Thr Ile Asp Gln Gly Leu
                   805                    810                    815
Phe Arg Asp Thr Ser Arg Leu Trp Arg Leu Phe Arg Glu Ile Leu Asp
                   820                    825                    830
```

19

```
Gly Leu Ala Tyr Ile His Glu Lys Gly Met Ile His Arg Asp Leu Lys
        835                 840                 845
Pro Val Asn Ile Phe Leu Asp Ser Asp Asp His Val Lys Ile Gly Asp
    850                 855                 860
Phe Gly Leu Ala Thr Asp His Leu Ala Phe Thr Ala Glu Gly Lys Gln
865                 870                 875                 880
Asp Asp Gln Ala Gly Asp Gly Val Ile Lys Ser Asp Pro Ser Gly His
                885                 890                 895
Leu Thr Gly Met Val Gly Thr Ala Leu Tyr Val Ser Pro Glu Val Gln
            900                 905                 910
Gly Ser Thr Lys Ser Ala Tyr Asn Gln Lys Val Asp Leu Phe Ser Leu
    915                 920                 925
Gly Ile Ile Phe Phe Glu Met Ser Tyr His Pro Met Val Thr Ala Ser
    930                 935                 940
Glu Arg Ile Phe Val Leu Asn Gln Leu Arg Asp Pro Thr Ser Pro Lys
945                 950                 955                 960
Phe Pro Asp Asp Phe Asp Asp Gly Glu His Thr Lys Gln Lys Ser Val
                965                 970                 975
Ile Ser Trp Leu Leu Asn His Asp Pro Ala Lys Arg Pro Thr Ala Met
            980                 985                 990
Glu Leu Leu Lys Ser Glu Leu Leu Pro Pro Pro Gln Met Glu Glu Ser
    995                 1000                1005
Glu Leu His Glu Val Leu His His Thr Leu Ala Asn Ile Asp Gly Lys
    1010                1015                1020
Ala Tyr Arg Thr Met Met Ser Gln Ile Phe Cys Gln His Ile Ser Pro
1025                1030                1035                1040
Ala Ile Asp Tyr Thr Tyr Asp Ser Asp Ile Leu Lys Gly Asn Phe Leu
                1045                1050                1055
Ile Arg Thr Ala Lys Ile Gln Gln Leu Val Cys Glu Thr Ile Val Arg
            1060                1065                1070
Val Phe Lys Arg His Gly Ala Val Gln Leu Cys Thr Pro Leu Leu Leu
            1075                1080                1085
Pro Arg Asn Arg Gln Ile Tyr Glu His Asn Glu Ala Ala Leu Phe Met
    1090                1095                1100
Asp His Ser Gly Met Leu Val Met Leu Pro Phe Asp Leu Arg Val Pro
1105                1110                1115                1120
Phe Ala Arg Tyr Val Ala Arg Asn Asn Ile Leu Asn Leu Lys Arg Tyr
                1125                1130                1135
Cys Ile Glu Arg Val Phe Arg Pro Arg Lys Leu Asp Arg Phe His Pro
            1140                1145                1150
Lys Glu Leu Leu Glu Cys Ala Phe Asp Ile Val Thr Ser Thr Thr Asn
    1155                1160                1165
Ser Ser Leu Pro Thr Ala Glu Thr Ile Tyr Thr Ile Tyr Glu Ile Ile
    1170                1175                1180
Gln Glu Phe Pro Ala Leu Gln Glu Arg Asn Tyr Ser Ile Tyr Leu Asn
1185                1190                1195                1200
His Thr Met Leu Leu Lys Ala Ile Leu Leu His Cys Gly Ile Pro Glu
            1205                1210                1215
Asp Lys Leu Ser Gln Val Tyr Val Ile Leu Tyr Asp Ala Val Thr Glu
            1220                1225                1230
Lys Leu Thr Arg Arg Glu Val Glu Ala Lys Phe Cys Asn Leu Ser Leu
    1235                1240                1245
Ser Ser Asn Ser Leu Cys Arg Leu Tyr Lys Phe Ile Glu Gln Lys Gly
    1250                1255                1260
Asp Leu Gln Asp Leu Thr Pro Thr Ile Asn Ser Leu Ile Lys Gln Lys
1265                1270                1275                1280
Thr Gly Val Ala Gln Leu Val Lys Tyr Ser Leu Lys Asp Leu Glu Asp
```

20

```
                    1285                  1290                  1295
         Val Val Gly Leu Leu Lys Lys Leu Gly Val Lys Leu Gln Val Ser Ile
                    1300                  1305                  1310
         Asn Leu Gly Leu Val Tyr Lys Val Gln Gln His Thr Gly Ile Ile Phe
                    1315                  1320                  1325
         Gln Phe Leu Ala Phe Ser Lys Arg Arg Gln Arg Val Val Pro Glu Ile
                    1330                  1335                  1340
         Leu Ala Ala Gly Gly Arg Tyr Asp Leu Leu Ile Pro Lys Phe Arg Gly
         1345                  1350                  1355                  1360
         Pro Gln Thr Val Gly Pro Val Pro Thr Ala Val Gly Val Ser Ile Ala
                    1365                  1370                  1375
         Ile Asp Lys Ile Phe Ala Val Val Leu Asn Met Glu Glu Pro Val Thr
                    1380                  1385                  1390
         Val Ser Ser Cys Asp Leu Leu Val Val Ser Val Gly Gln Met Ser Met
                    1395                  1400                  1405
         Ser Arg Ala Ile Asn Leu Thr Gln Lys Leu Trp Thr Ala Gly Ile Thr
                    1410                  1415                  1420
         Ala Glu Ile Met Tyr Asp Trp Ser Gln Ser Gln Glu Glu Leu Gln Glu
         1425                  1430                  1435                  1440
         Tyr Cys Arg His His Glu Ile Thr Tyr Val Ala Leu Val Ser Asp Lys
                    1445                  1450                  1455
         Glu Gly Ser His Val Lys Val Lys Ser Phe Glu Lys Glu Arg Gln Thr
                    1460                  1465                  1470
         Glu Lys Arg Val Leu Glu Ser Asp Leu Val Asp His Val Met Gln Lys
                    1475                  1480                  1485
         Leu Arg Thr Lys Val Gly Asp Glu Arg Asn Phe Arg Asp Ala Ser Asp
                    1490                  1495                  1500
         Asn Leu Ala Val Gln Thr Leu Lys Gly Ser Phe Ser Asn Ala Ser Gly
         1505                  1510                  1515                  1520
         Leu Phe Glu Ile His Gly Thr Thr Val Val Pro Asn Val Ile Val Leu
                    1525                  1530                  1535
         Ala Pro Glu Lys Leu Ser Ala Ser Thr Arg Arg Arg His Glu Ile Gln
                    1540                  1545                  1550
         Val Gln Thr Arg Leu Gln Thr Thr Leu Ala Asn Leu His Gln Lys Ser
                    1555                  1560                  1565
         Ser Glu Ile Glu Ile Leu Ala Val Asp Leu Pro Lys Glu Thr Ile Leu
                    1570                  1575                  1580
         Gln Phe Leu Ser Leu Glu Trp Asp Ala Asp Glu Gln Ala Phe Asn Thr
         1585                  1590                  1595                  1600
         Thr Val Lys Gln Leu Leu Ser Arg Leu Pro Lys Gln Arg Tyr Leu Lys
                    1605                  1610                  1615
         Leu Val Cys Asp Glu Ile Tyr Asn Ile Lys Val Glu Lys Lys Val Ser
                    1620                  1625                  1630
         Val Leu Phe Leu Tyr Ser Tyr Arg Asp Asp Tyr Tyr Arg Ile Leu Phe
                    1635                  1640                  1645
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<210> 6
<211> 270
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<221> VARIANT
<222> (1)...(270)
<223> Xaa = Any Amino Acid

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<400> 6
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Gly Xaa Xaa Xaa Xaa
 1               5                   10              15
Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Xaa
             20                  25                  30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
         35                  40                  45
Xaa Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
     50                  55                  60
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65                  70                  75                  80
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
             85                  90                  95
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
             100                 105                 110
Xaa Xaa Xaa Xaa His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa His Arg Asp
         115                 120                 125
Xaa Lys Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
     130                 135                 140
Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Xaa Asp Phe Gly Xaa Xaa Xaa Xaa
145                 150                 155                 160
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
             165                 170                 175
Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp
         180                 185                 190
Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
         195                 200                 205
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
     210                 215                 220
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
225                 230                 235                 240
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa Xaa Xaa
             245                 250                 255
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa His Xaa Xaa Xaa
             260                 265                 270

<210> 7
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<221> VARIANT
<222> (1)...(30)
<223> Xaa = Any Amino Acid

<400> 7
Gly Xaa Gly Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1               5                   10                  15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys
             20                  25                  30

<210> 8
<211> 105
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22

<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 8
Ile Leu Lys Lys Glu Ser Leu Ser Leu Arg Glu Ile Gln Ile Leu Lys
1   5   10   15
Arg Leu Ser His Pro Asn Ile Val Arg Leu Leu Gly Val Phe Glu Asp
            20   25   30
Thr Asp Asp His Leu Tyr Leu Val Met Glu Tyr Met Glu Gly Gly Asp
            35   40   45
Leu Phe Asp Tyr Leu Arg Arg Asn Gly Pro Leu Ser Glu Lys Glu Ala
    50   55   60
Lys Lys Ile Ala Leu Gln Ile Leu Arg Gly Leu Glu Tyr Leu His Ser
65   70   75   80
Asn Gly Ile Val His Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp
                85   90   95
Glu Asn Gly Thr Val Lys Ile Ala Asp
            100   105

<210> 9
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 9
Arg Leu Pro Leu Pro Ser Asn Cys Ser Glu Glu Leu Lys Asp Leu Leu
1   5   10   15
Lys Lys Cys Leu Asn Lys Asp Pro Ser Lys Arg Pro Gly Ser Ala Thr
            20   25   30
Ala Lys Glu Ile Leu Asn His Pro Gln Phe
            35   40

<210> 10
<211> 66
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 10
Tyr Glu Leu Leu Glu Lys Leu Gly Glu Gly Ser Phe Gly Lys Val Tyr
1   5   10   15
Lys Ala Lys His Lys Thr Gly Lys Ile Val Ala Val Lys Ile Leu Lys
            20   25   30
Lys Glu Ser Leu Ser Leu Arg Glu Ile Gln Ile Leu Lys Arg Leu Ser
            35   40   45
His Pro Asn Ile Val Arg Leu Leu Gly Val Phe Glu Asp Thr Asp Asp
    50   55   60
His Leu
65

23

<210> 11
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 11
His Leu Tyr Leu Val Met Glu Tyr Met Glu Gly Gly Asp Leu Phe Asp
1   5   10   15
Tyr Leu Arg Arg Asn Gly Pro Leu Ser Glu Lys Glu Ala Lys Lys Ile
            20   25   30
Ala Leu Gln Ile Leu Arg Gly Leu Glu Tyr Leu His Ser Asn Gly Ile
        35   40   45
Val His Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp Glu Asn Gly
    50   55   60
Thr Val Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Leu Glu Lys Leu
65   70   75   80
Thr Thr Phe Val Gly Thr Pro Trp Tyr Met Met Ala Pro Glu Val Ile
                85   90   95
Leu Glu Gly Arg Gly Tyr Ser Ser Lys Val Asp Val Trp Ser Leu Gly
            100   105   110
Val Ile Leu Tyr Glu Leu Leu Thr Gly Gly Pro Leu Phe Pro Gly Ala
        115   120   125
Asp Leu Pro Ala Phe Thr Gly Gly Asp Glu Val Asp Gln Leu Ile Ile
    130   135   140
Phe Val Leu Lys Leu Pro Phe Ser Asp Glu Leu Pro Lys Thr Arg Ile
145   150   155   160
Asp Pro Leu Glu Glu Leu Phe Arg Ile Lys Lys Arg Arg Leu Pro Leu
                165   170   175
Pro Ser Asn Cys Ser Glu Glu Leu Lys Asp Leu Leu Lys Lys Cys Leu
            180   185   190
Asn Lys Asp Pro Ser Lys Arg Pro Gly Ser Ala Thr Ala Lys Glu Ile
            195   200   205
Leu Asn His Pro Gln Phe
            210

<210> 12
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 12
Thr Asp Ile Ile Lys Tyr Pro Val Ile Thr Glu Lys Leu Ala Met Asn
1   5   10   15
Leu Leu Glu Glu Pro Asn Lys
            20

<210> 13
<211> 504
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 13

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Asn Gln Thr Thr Glu Arg Val Tyr Glu Leu His Lys Ile Glu Leu Phe
1               5                   10                  15
Ser Val Pro Glu Leu Asn Gly Lys Lys Ile Gly Leu Gly Ile Lys Leu
            20                  25                  30
Pro Lys Thr Asp Thr Glu Ser Leu Arg Thr Met Val Ala Lys Leu Leu
        35                  40                  45
Gly Leu Ala Met Lys Thr Lys Thr Phe Pro Asp Asp Glu Gly Ser Gln
    50                  55                  60
Pro Val Ser Phe Glu Arg Lys Asp Leu Glu Glu Ser Leu Lys Glu Lys
65                  70                  75                  80
Asp Tyr Phe Val Cys Glu Lys Thr Asp Gly Ile Arg Cys Ser His Gly
            85                  90                  95
Phe Asn Arg Thr Gly Phe Leu Ile Ala Ala Leu Leu Phe Leu Val Glu
        100                 105                 110
His Pro Gly Leu Glu Glu Ala Ile Ser His Ile Leu Ser Gly Glu Phe
    115                 120                 125
Leu Ile Asp Arg Glu Lys Asn Tyr Tyr Lys Gln Asp Tyr Ile Asp Leu
    130                 135                 140
Leu Pro Lys Arg Leu Phe Pro Arg Glu Lys Asp Lys Thr Lys Ala Lys
145                 150                 155                 160
Glu Leu Pro Thr Tyr His Arg Gly Thr Leu Leu Asp Gly Glu Leu Val
            165                 170                 175
Ile Asp Ile Asn Arg Ile Ala Val Glu Gln Lys Thr Leu Arg Tyr Val
            180                 185                 190
Val Phe Asp Ala Leu Ala Ile Ser Gly Gln Thr Val Ile Gln Arg Asp
        195                 200                 205
Leu Ser Lys Arg Leu Gly Asp Glu Phe Ile Lys Ala Val Lys Lys Pro
    210                 215                 220
Phe Asp Glu Phe Lys Lys Val Met Pro Asp Ala Lys Ile Leu Asn Gln
225                 230                 235                 240
Gln Lys Tyr Asn Phe Pro Phe Lys Ile Gly Leu Lys His Met Ser Leu
            245                 250                 255
Ser Tyr Gly Gln Leu Lys Leu Leu Lys Ala Glu Ser Lys Met Val Ile
            260                 265                 270
Ser Lys Ala Asp Ala Met Pro Lys Leu Leu His Ile Asn Asp Gly Leu
    275                 280                 285
Ile Phe Thr Cys Val Arg Asp Thr Pro Tyr Ile Glu Gly Glu Ile Leu
    290                 295                 300
Val Glu Pro Gly Asn Ser Tyr Leu Asp Phe Asn Leu Leu Lys Trp Lys
305                 310                 315                 320
Pro Lys Glu Glu Asn Thr Val Asp Phe Glu Leu Ile Leu Glu Phe Glu
            325                 330                 335
Glu Val Asn Asp Pro Glu Leu Asp Glu Lys Asp Gly Phe Ser Leu Tyr
            340                 345                 350
Leu Asp Tyr Asp Ala Met Pro Gly Glu Leu Phe Lys Phe Ser Leu Gly
    355                 360                 365
Val Trp Gln Gly Gly Phe Asn Lys Arg Phe Glu Val Ile His Thr Asp
    370                 375                 380
Gln Ile Phe Phe Arg Val Ala Phe Gln Lys Leu Gly Arg Leu Lys His
385                 390                 395                 400
Glu Phe Ala Glu Leu Ser Val Ser Asp Lys Asp Trp Tyr Lys Leu Lys
            405                 410                 415
```

25

```
Ala Leu Glu Gln Pro Leu Asp Gly Arg Ile Val Glu Cys Arg Leu Ala
            420                 425                 430
Asp Ile Glu Ile Leu Ile Phe Gln Glu Gly Arg Trp Glu Tyr Leu Arg
            435                 440                 445
Phe Arg Asp Asp Lys Gln Gln Ala Leu Lys Thr Gly Gly Tyr Ser Gly
    450                 455                 460
Asn His Ile Ser Thr Val Glu Lys Val Leu Leu Ser Ile Lys Asp Gly
465                 470                 475                 480
Val Ser Ile Glu Glu Leu Leu Lys Leu Phe Pro Gly Met Tyr Phe Ala
            485                 490                 495
Gly Ala Lys Thr Leu Ile Lys Arg
            500


<210> 14
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 14
Tyr Glu Leu Leu Lys Lys Leu Gly Lys Gly Ala Phe Gly Lys Val Tyr
 1               5                  10                  15
Leu Ala Arg Asp Lys Lys Thr Gly Arg Leu Val Ala Ile Lys Val Ile
            20                  25                  30
Lys Glu Arg Ile Leu Arg Glu Ile Lys Ile Leu Lys Lys Asp His Pro
            35                  40                  45
Asn Ile Val Lys Leu Tyr Asp Val Phe Glu Asp Asp Lys Leu Tyr Leu
    50                  55                  60
Val Met Glu Tyr Cys Glu Gly Asp Leu Gly Asp Leu Phe Asp Leu Leu
65                  70                  75                  80
Lys Lys Arg Gly Arg Arg Gly Leu Arg Lys Val Leu Ser Glu Glu Ala
            85                  90                  95
Arg Phe Tyr Phe Arg Gln Ile Leu Ser Ala Leu Glu Tyr Leu His Ser
            100                 105                 110
Gln Gly Ile Ile His Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp
            115                 120                 125
Ser His Val Lys Leu Ala Asp Phe Gly Leu Ala Arg Gln Leu Thr Thr
    130                 135                 140
Phe Val Gly Thr Pro Glu Tyr Met Ala Pro Glu Val Leu Gly Tyr Gly
145                 150                 155                 160
Lys Pro Ala Val Asp Ile Trp Ser Leu Gly Cys Ile Leu Tyr Glu Leu
            165                 170                 175
Leu Thr Gly Lys Pro Pro Phe Pro Gln Leu Asp Leu Ile Phe Lys Lys
            180                 185                 190
Ile Gly Ser Pro Glu Ala Lys Asp Leu Ile Lys Lys Leu Leu Val Lys
            195                 200                 205
Asp Pro Glu Lys Arg Leu Thr Ala Glu Ala Leu Glu Asp Glu Leu Asp
    210                 215                 220
Ile Lys Ala His Pro Phe Phe
225                 230


<210> 15
<211> 231
<212> PRT
<213> Artificial Sequence
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26

<220>
<223> Consensus kinase sequence

<400> 15

```
Tyr Glu Leu Leu Lys Lys Leu Gly Lys Gly Ala Phe Gly Lys Val Tyr
1                 5                   10                  15
Leu Ala Arg Asp Lys Lys Thr Gly Arg Leu Val Ala Ile Lys Val Ile
              20                  25                  30
Lys Glu Arg Ile Leu Arg Glu Ile Lys Ile Leu Lys Lys Asp His Pro
          35                  40                  45
Asn Ile Val Lys Leu Tyr Asp Val Phe Glu Asp Asp Lys Leu Tyr Leu
    50                  55                  60
Val Met Glu Tyr Cys Glu Gly Asp Leu Gly Asp Leu Phe Asp Leu Leu
65                  70                  75                  80
Lys Lys Arg Gly Arg Arg Gly Leu Arg Lys Val Leu Ser Glu Glu Ala
              85                  90                  95
Arg Phe Tyr Phe Arg Gln Ile Leu Ser Ala Leu Glu Tyr Leu His Ser
            100                 105                 110
Gln Gly Ile Ile His Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp
        115                 120                 125
Ser His Val Lys Leu Ala Asp Phe Gly Leu Ala Arg Gln Leu Thr Thr
    130                 135                 140
Phe Val Gly Thr Pro Glu Tyr Met Ala Pro Glu Val Leu Gly Tyr Gly
145                 150                 155                 160
Lys Pro Ala Val Asp Ile Trp Ser Leu Gly Cys Ile Leu Tyr Glu Leu
              165                 170                 175
Leu Thr Gly Lys Pro Pro Phe Pro Gln Leu Asp Leu Ile Phe Lys Lys
              180                 185                 190
Ile Gly Ser Pro Glu Ala Lys Asp Leu Ile Lys Lys Leu Leu Val Lys
        195                 200                 205
Asp Pro Glu Lys Arg Leu Thr Ala Glu Ala Leu Glu Asp Glu Leu Asp
    210                 215                 220
Ile Lys Ala His Pro Phe Phe
225                 230
```

<210> 16
<211> 280
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 16

```
Leu Thr Leu Gly Lys Lys Leu Gly Glu Gly Ala Phe Gly Glu Val Tyr
1                 5                   10                  15
Lys Gly Thr Leu Lys Ile Glu Val Ala Val Lys Thr Leu Lys Glu Asp
              20                  25                  30
Ala Lys Glu Glu Phe Leu Arg Glu Ala Lys Ile Met Lys Lys Leu Gly
          35                  40                  45
Gly Lys His Pro Asn Ile Val Lys Leu Leu Gly Val Cys Thr Glu Glu
    50                  55                  60
Gly Arg Arg Phe Met Glu Val Glu Pro Leu Met Ile Val Met Glu Tyr
65                  70                  75                  80
Met Glu Gly Gly Asp Leu Leu Asp Tyr Leu Arg Lys Asn Arg Pro Lys
              85                  90                  95
```

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Leu Ser Leu Ser Asp Leu Leu Ser Phe Ala Leu Gln Ile Ala Lys Gly
            100   105   110
Met Glu Tyr Leu Glu Ser Lys Asn Phe Val His Arg Asp Leu Ala Ala
            115   120   125
Arg Asn Cys Leu Val Gly Glu Asn Lys Val Val Lys Ile Ser Asp Phe
            130   135   140
Gly Leu Ser Arg Asp Leu Tyr Asp Asp Asp Lys Lys Gly Glu Ser Lys
145   150   155   160
Asp Tyr Tyr Arg Lys Lys Gly Gly Lys Gly Gly Lys Thr Leu Leu Pro
                165   170   175
Ile Arg Trp Met Ala Pro Glu Ser Leu Lys Asp Gly Lys Phe Thr Ser
                180   185   190
Lys Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu Ile Phe Thr
            195   200   205
Leu Gly Glu Gln Pro Tyr Pro Gly Glu Ile Gln Gln Phe Met Ser Asn
            210   215   220
Glu Glu Val Leu Glu Tyr Leu Lys. Lys Gly Tyr Arg Leu Pro Lys Pro
225   230   235   240
Glu Asn Asp Leu Pro Ile Ser Ser Val Thr Cys Pro Asp Glu Leu Tyr
                245   250   255
Asp Leu Met Leu Gln Cys Trp Ala Glu Asp Pro Glu Asp Arg Pro Thr
            260   265   270
Phe Ser Glu Leu Val Glu Arg Leu
            275   280

<210> 17
<211> 144
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 17
Ser Phe Arg Glu Arg Gln Ala Gln Glu Leu Glu Val Ile Lys Ser Ile
  1   5   10   15
Phe Gly Cys Asp Val Glu Asp Leu Arg Pro Gln Ala Asn Pro Ser Leu
            20   25   30
Trp Lys Pro Thr Asp Ile Arg Ile Gln Leu Thr Pro Leu Arg Asp Ser
            35   40   45
Ser Asn Gly Leu Glu Thr Tyr Val Cys Thr Lys Leu His Val Thr Cys
            50   55   60
Pro Ser Lys Tyr Pro Lys Leu Pro Pro Lys Ile Ser Leu Glu Glu Ser
65   70   75   80
Lys Gly Met Ser Asp Gln Leu Leu Glu Ala Leu Arg Asn Gln Leu Gln
                85   90   95
Ala Gln Ser Gln Glu Leu Arg Gly Glu Val Met Ile Tyr Glu Leu Ala
            100   105   110
Gln Thr Val Gln Ala Phe Leu Leu Glu His Asn Lys Pro Pro Lys Gly
            115   120   125
Ser Phe Tyr Asp Gln Met Leu Gln Asp Lys Gln Lys Arg Asp Gln Glu
            130   135   140

<210> 18
<211> 54
<212> PRT
<213> Artiicial sequence

<220>
<223> Consensus kinase sequence

<400> 18
Glu Thr Leu Tyr Phe His Lys Met Gly Arg Gln Ile Gln Arg Gly Cys
1   5   10   15
Cys Val Gly His Ser Gln Arg Gly Cys Ile Ala Tyr Thr Gly Ile Asp
            20   25   30
Met His Cys Gly Gln Leu Leu Tyr Ile Thr Glu Trp Asn Ile Lys Tyr
        35   40   45
Ser Gln Leu Glu Gln Pro
    50

<210> 19
<211> 332
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 19
Leu Lys Ser Leu Met Arg Gly Lys Gly Glu Ala Ala Ser Leu Ala Arg
1   5   10   15
Gly Ala Leu Arg Glu Leu Glu Thr Val Val Gly Leu Ala Tyr Ser Leu
            20   25   30
Gly Val Lys Cys Pro Ile His Ile Trp Ala Gly Leu Pro Ile Ser Phe
        35   40   45
Asp Arg Ala Ser Asn Gly Gly Ile Val Trp Gln Met Thr Ala Asp Leu
    50   55   60
Lys Pro Asn Arg Ser Gly His Pro Ser Val Leu Ala Ile Gly Glu Arg
65   70   75   80
Tyr Asp Ser Met Leu His Glu Phe Gln Lys Gln Ala Gln Lys Phe Asn
            85   90   95
Pro Ala Met Pro Ala Arg Gly Val Leu Ser Gly Ala Gly Leu Thr Phe
            100   105   110
Ser Leu Asp Lys Leu Val Ala Ala Val Gly Val Glu Tyr Ala Lys Asp
        115   120   125
Cys Arg Ala Ile Asp Val Gly Ile Cys Val Cys Gly Thr Arg Pro Pro
    130   135   140
Leu Lys Asp Val Thr Tyr Ile Met Arg Leu Leu Trp Ser Val Gly Ile
145   150   155   160
Arg Cys Gly Ile Val Glu Ala Ala Ser Glu Leu Gly Asp Glu Ala Gln
                165   170   175
Asp Leu Ala Arg Leu Gly Ala Leu His Val Ile Leu Val Ala Glu Asn
            180   185   190
Gly Ser Leu Arg Val Arg Ser Phe Glu Arg Glu Arg Phe Gln Glu Arg
        195   200   205
His Leu Thr Arg Thr Glu Leu Val Glu Phe Ile Gln Lys Met Leu Arg
    210   215   220
Ser Asp Gly Leu Asn Gly Thr Thr Val Asp Asn Phe Ser His Leu Ser
225   230   235   240
Ala Leu Gly Ser Gly Asp Asn Arg Ser Ser Gly Gly Lys Glu Arg Glu
                245   250   255
Arg Gly Glu Asn Gly Leu Ser Thr Ser Ala Ser Asn Ala Thr Ile Lys
                260   265   270

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Asn Asn Tyr Ser Gln Leu Pro Asn Leu Gln Val Thr Phe Leu Thr His
        275   280   285
Asp Lys Pro Thr Ala Asn Tyr Lys Arg Arg Leu Glu Asn Gln Val Ala
        290   295   300
Gln Gln Met Ser Ser Thr Leu Ser Gln Phe Leu Lys Lys Glu Thr Phe
305   310   315   320
Val Val Leu Val Val Glu Leu Pro Pro Ala Val Val
                325   330

<210> 20
<211> 296
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 20
Val Leu Ser Gly Ala Gly Leu Thr Phe Ser Leu Asp Lys Leu Val Ala
1   5   10   15
Ala Val Gly Val Glu Tyr Ala Lys Asp Cys Arg Ala Ile Asp Val Gly
            20   25   30
Ile Cys Val Cys Gly Thr Arg Pro Pro Leu Lys Asp Val Thr Tyr Ile
            35   40   45
Met Arg Leu Leu Trp Ser Val Gly Ile Arg Cys Gly Ile Val Glu Ala
        50   55   60
Ala Ser Glu Leu Gly Asp Glu Ala Gln Asp Leu Ala Arg Leu Gly Ala
65   70   75   80
Leu His Val Ile Leu Val Ala Glu Asn Gly Ser Leu Arg Val Arg Ser
            85   90   95
Phe Glu Arg Glu Arg Phe Gln Glu Arg His Leu Thr Arg Thr Glu Leu
            100   105   110
Val Glu Phe Ile Gln Lys Met Leu Arg Ser Asp Gly Leu Asn Gly Thr
            115   120   125
Thr Val Asp Asn Phe Ser His Leu Ser Ala Leu Gly Ser Gly Asp Asn
        130   135   140
Arg Ser Ser Gly Gly Lys Glu Arg Glu Arg Gly Glu Asn Gly Leu Ser
145   150   155   160
Thr Ser Ala Ser Asn Ala Thr Ile Lys Asn Asn Tyr Ser Gln Leu Pro
            165   170   175
Asn Leu Gln Val Thr Phe Leu Thr His Asp Lys Pro Thr Ala Asn Tyr
            180   185   190
Lys Arg Arg Leu Glu Asn Gln Val Ala Gln Gln Met Ser Ser Thr Leu
        195   200   205
Ser Gln Phe Leu Lys Lys Glu Thr Phe Val Val Leu Val Val Glu Leu
        210   215   220
Pro Pro Ala Val Val Asn Ala Ile Val Gly Ala Ile Asn Pro Arg Glu
225   230   235   240
Ile Arg Lys Arg Glu Thr Glu Pro Glu Ile Asn Tyr Val Ile Glu Arg
            245   250   255
Phe Ser Lys Tyr Lys Arg Tyr Ile Ser Glu Ile Asn Glu Glu Val Val
            260   265   270
Asp Tyr Leu Ser Asp Ala Lys Thr Pro Ile Val Ala Leu Tyr Ser Ile
        275   280   285
Ser Asp Ser Tyr Tyr Arg Val Ile
        290   295

<210> 21
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 21
Asp Gln Gly Gly Glu Leu Leu Ser Leu Arg Tyr Asp Leu Thr Val Pro
 1   5   10   15
Phe Ala Arg Tyr Val Ala Met Asn Leu Leu Lys Val Thr Asn Leu Pro
            20   25   30
Leu Lys Arg Tyr His Ile Ala Lys Val Tyr Arg Arg Asp Arg Pro Ala
            35   40   45
Met Thr Arg Gly Arg Tyr Arg Glu Phe Tyr Gln Cys Asp Phe Asp Ile
    50   55   60
Ile Gly Glu Tyr Asp Thr Met Ala Pro Asp Ala Glu Ile Leu Lys Ile
65   70   75   80
Leu Thr Glu Ile Leu Ser Gln Leu Gly Ile Arg Glu Leu Gly Asn Phe
                85   90   95
Lys Ile Lys Ile Asn His Arg Gly Ile Leu Asp Ser Leu Leu Gln Pro
            100   105   110
Trp Pro Lys Thr Leu Gln Glu Tyr Leu Thr Gln Tyr Lys Ala
            115   120   125

<210> 22
<211> 104
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 22
Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp Glu Glu Ser His Glu Asn
 1   5   10   15
Thr Pro Asn Met Ile Lys Leu Ile Ala Asp Phe Gly Leu Ala Lys Glu
            20   25   30
Ile Tyr Ser Ser Ser Ser Thr Tyr Glu Glu Met Ser Ser Ser Gln Ala
            35   40   45
Val Phe Gly Ser His Gln Thr Thr Ser Thr Met Cys Gly Thr Pro Tyr
    50   55   60
Tyr Val Ser Met Lys Ser Met Ala Pro Glu Tyr Met Ala Pro Glu Ser
65   70   75   80
Ser Ala Thr Asn Tyr Gln Lys Tyr Ser Thr Lys Ser Asp Val Trp Ser
            85   90   95
Phe Gly Val Ile Leu Tyr Glu Met
            100

<210> 23
<211> 100
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

31

<400> 23

```
Gln Leu Met His Tyr Val His Gln Ile Ala Lys Gly Leu Glu Tyr Leu
1               5                   10                  15
His Ser Lys Asn Gln Lys His Gln Gly Ile Ile His Arg Ala Lys Lys
            20                  25                  30
Val Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp Glu Glu Ser His Glu
            35                  40                  45
Asn Thr Pro Asn Met Ile Lys Leu Ile Ala Asp Phe Gly Leu Ala Lys
        50                  55                  60
Glu Ile Tyr Ser Ser Ser Ser Thr Tyr Glu Glu Met Ser Ser Ser Gln
65                      70                  75                  80
Ala Val Phe Gly Ser His Gln Thr Thr Ser Thr Met Cys Gly Thr Pro
                85                  90                  95
Tyr Tyr Val Ser
            100
```

<210> 24
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 24

```
Glu Gly Ser Leu Val Glu Tyr Met Glu Tyr Met Ser Gly Gly Ser Glu
1               5                   10                  15
Asp Tyr Met Lys Lys Leu Ser Leu Glu Thr Val Met Lys Ile Ala Met
            20                  25                  30
Met Ile Leu Gln Phe Met Gln Ile Met His Met Ser Ser Glu Ser Glu
            35                  40                  45
Ser Leu Ser His Ser Gln Leu Met His Tyr Val His Gln Ile Ala Lys
        50                  55                  60
Gly Leu Glu Tyr Leu His Ser Lys Asn Gln Lys His Gln Gly Ile Ile
65                      70                  75                  80
His Arg Ala Lys Lys Val Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp
                85                  90                  95
Glu Glu Ser His Glu Asn Thr Pro Asn Met Ile Lys Leu Ile Ala Asp
                100                 105                 110
Phe Gly Leu Ala Lys Glu Ile
            115
```

<210> 25
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 25

```
Tyr Met Ala Pro Glu Ser Ser Ala Thr Asn Tyr Gln Lys Tyr Ser Thr
1               5                   10                  15
Lys Ser Asp Val Trp Ser Phe Gly Val Ile Leu Tyr Glu Met Leu Thr
            20                  25                  30
Gly Lys Pro Pro Phe Phe Pro Gly Glu Ser Glu Val Ser Glu Glu Glu
```

```
                35                      40                      45
Pro Tyr Gln Ser Met Lys Asn Met Glu Val Leu Glu Met Gly Pro Glu
        50                      55                      60
Glu Thr Ile Gln Lys Val Met Ser Lys Ile Val Glu Lys Lys Gly Glu
65                      70                      75                      80
Arg Met Pro Gln Pro Ser Ser Ser Asn Cys Pro Glu Val Ser Gln Glu
                85                      90                      95
Ala Lys Asp Leu Leu Lys Lys Cys Leu Gln Lys Asp Pro Glu Lys Arg
                100                     105                     110
Arg Pro Thr Phe Glu Glu Ile Leu Gln His
                115                     120
```

<210> 26
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 26
```
Gln Tyr Glu Leu Leu Lys Lys Leu Leu Gly Lys Gly Ser Phe Gly Lys
1                   5                   10                      15
Val Tyr Lys Ala Lys His Lys
                20
```

<210> 27
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 27
```
Glu Val Ser Gln Glu Ala Lys Asp Leu Leu Lys Lys Cys Leu Gln Lys
1                   5                   10                      15
Asp Pro Glu Lys Arg Arg Pro Thr Phe Glu Glu Ile Leu Gln His Pro
                20                      25                      30
Trp Phe Leu Met Arg Asn Pro
                35
```

<210> 28
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 28
```
Leu Gly Thr Gly Ser Phe Gly Ala Val Tyr Lys
1                   5                   10
```

<210> 29
<211> 104
<212> PRT

<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 29

```
Leu Asp Gln Asn Gly Thr Val Leu Gln Leu Pro Phe Asp Leu Met Met
1               5                   10                  15
Gly His Ala Arg Ser Leu Ala Arg Ile Thr Asn Ser Pro Val Val Gln
                20                  25                  30
Lys Ser Tyr Ser Phe Gly Asn Ile Phe Arg Asp Arg His Gly Gly Gly
            35                  40                  45
Gln Pro Asp Val Tyr Gly Glu Val Asp Phe Asp Ile Val Thr Ser Asp
        50                  55                  60
Ala Leu Asp Leu Ala Leu Lys Glu Ala Glu Val Ile Lys Val Leu Asp
65                  70                  75                  80
Glu Ile Ala Thr Ala Phe Pro Thr Val Ser Ser Thr Pro Ile Cys Phe
                85                  90                  95
Gln Leu Gly His Ser Asp Leu Leu
                100
```

<210> 30
<211> 151
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 30

```
Tyr Gln Glu Val Gln Glu Ser Glu Val Met Val Leu Gln Ala Ile Tyr
1               5                   10                  15
Gly Glu Asp Phe Thr Gln His Glu Ala Ala His Gly Ala Trp Gln Lys
                20                  25                  30
Ser Glu Pro Arg Phe Asp Ile Lys Ile Lys Pro Ser Ser Asp Gln Glu
            35                  40                  45
Leu Ser Val Thr Leu Gly Val Val Met Val Ala Thr Tyr Pro Lys Thr
        50                  55                  60
Pro Pro Leu Leu Thr Ile Lys Asp Asp His Ser Leu Arg Glu Ser Thr
65                  70                  75                  80
Lys Phe Lys Ile Gln Lys Phe Val Glu Thr Gln Pro Lys Ile Tyr Ala
                85                  90                  95
Gln Ala Glu Gln Glu Met Ile Asp Gln Ile Val Glu Gly Ile Arg Asp
                100                 105                 110
Ile Leu Glu Glu Ala Ala Gln Lys Lys Val Gln Gly Leu Glu Ile Pro
            115                 120                 125
Ser Leu Glu Glu Glu Arg Ala Ala His Glu Ala Glu Leu Ala Arg Leu
        130                 135                 140
Ala Gln Ser Glu Lys Glu Arg
145                 150
```

<210> 31
<211> 48
<212> PRT
<213> Artificial Sequence

<220>

34

<223> Consensus kinase sequence

<400> 31
Glu Ala Glu Leu Ala Arg Leu Ala Gln Ser Glu Lys Glu Arg Glu Glu
1   5   10   15
Arg Lys Lys Leu Glu Glu Ser Lys Glu Glu Glu Arg Val Leu Glu Asp
            20   25   30
Met Leu Gln Glu Glu Leu Lys Arg Gln Arg Asn Lys Ala Lys Glu Ser
        35   40   45

<210> 32
<211> 59
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 32
Arg Asn Lys Ala Lys Glu Ser Arg Lys Lys Asn Arg Ser His Gln Leu
1   5   10   15
Ser Pro Asp Arg Ala Pro Gln Asp Pro Gly Glu Thr Asp Glu Thr Leu
            20   25   30
Met Phe Asp Gln Pro Cys Lys Ile Thr Asp Gly Ser Gly Asn Ala Leu
        35   40   45
Phe Phe Gln Thr Val Ile Gly Lys Thr Val Phe
        50   55

<210> 33
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus kinase sequence

<400> 33
Leu Glu Glu Ser Lys Glu Glu Glu Arg Val Leu Glu Asp Met Leu Gln
1   5   10   15
Glu Glu Leu Lys Arg Gln Arg Asn Lys Ala Lys Glu Ser Arg Lys Lys
            20   25   30
Asn Arg Ser His Gln Leu Ser Pro Asp Arg Ala Pro Gln Asp Pro Gly
        35   40   45
Glu Thr Asp Glu Thr Leu Met Phe Asp Gln Pro Cys Lys Ile Thr Asp
        50   55   60
Gly Ser Gly Asn Ala Leu Phe Phe Gln Thr Val Ile Gly Lys Thr Val
65   70   75   80
Phe Arg Glu